

SEARCH REQUEST FORM

Scientific and Technical Information Center

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 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
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If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
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STAFF USE ONLY**Type of Search****Vendors and cost where applicable**

| | | |
|---|---|--|
| Searcher: <u>Jan</u> | NA Sequence (#) _____ | STN _____ |
| Searcher Phone #: <u>4448</u> | AA Sequence (#) <input checked="" type="checkbox"/> | Dialog _____ |
| Searcher Location: _____ | Structure (#) _____ | Questel/Orbit _____ |
| Date Searcher Picked Up: <u>5/27/03</u> | Bibliographic _____ | Dr. Link _____ |
| Date Completed: <u>5/28/03</u> | Litigation _____ | Lexis/Nexis _____ |
| Searcher Prep & Review Time: _____ | Fulltext _____ | Sequence Systems <input checked="" type="checkbox"/> |
| Clerical Prep Time: <u>10</u> | Patent Family _____ | WWW/Internet _____ |
| Online Time: <u>10</u> | Other _____ | Other (specify) _____ |

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 27, 2003, 18:24:51 : Search time 36 Seconds
(without alignments)
869,830 Million cell updates/sec

Title: US-08-994-468-6
Perfect score: 1242
Sequence: 1 MVTLPAPMSPTTYLLLL... RRGCVPPVPSODLLVEH 235

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_101002:*

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- 2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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- 10: /SID2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
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- 20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|----------------------|
| 1 | 1242 | 100.0 | 235 | AA67541 | Human flt-3 ligand |
| 2 | 1242 | 100.0 | 235 | AA67769 | Human flt-3 ligand |
| 3 | 1242 | 100.0 | 235 | AA67919 | Full length wild t |
| 4 | 1242 | 100.0 | 235 | AA680192 | Human flt-3 ligand |
| 5 | 1242 | 100.0 | 235 | AA680129 | Human flt-3 ligand |
| 6 | 1236 | 99.5 | 235 | AA66175 | Human S86/S109 flt |
| 7 | 1236 | 99.5 | 235 | AA620194 | Human flt-3 ligand |
| 8 | 1124 | 90.5 | 212 | AA67921 | Human flt-3 ligand |
| 9 | 1114 | 89.7 | 209 | AA67907 | Human flt-3 receptor |
| 10 | 1114 | 89.7 | 209 | AA67920 | Mature wild type h |

| | | | | | | |
|----|-------|------|-----|----|----------|----------------------|
| 11 | 1110 | 89.4 | 209 | 21 | AA67923 | Human flt-3 mutin |
| 12 | 1110 | 89.4 | 209 | 21 | AA67926 | Human flt-3 mutin |
| 13 | 1110 | 89.4 | 209 | 21 | AA67927 | Human flt-3 mutin |
| 14 | 1110 | 89.4 | 209 | 21 | AA67929 | Human flt-3 mutin |
| 15 | 1108 | 89.2 | 209 | 21 | AA67922 | Human flt-3 mutin |
| 16 | 1108 | 89.2 | 209 | 21 | AA67924 | Human flt-3 mutin |
| 17 | 1107 | 89.1 | 209 | 21 | AA67928 | Human flt-3 mutin |
| 18 | 1100 | 88.6 | 209 | 21 | AA67925 | Human flt-3 mutin |
| 19 | 970 | 78.1 | 185 | 22 | AA620195 | Human flt-3 ligand |
| 20 | 895.5 | 72.1 | 294 | 21 | AA678204 | Canine flt-3 ligand |
| 21 | 894.5 | 72.0 | 291 | 21 | AA678210 | Canine flt-3 ligand |
| 22 | 834 | 67.1 | 178 | 22 | AA620193 | Human flt-3 ligand |
| 23 | 797.5 | 64.2 | 268 | 21 | AA658206 | Canine mature flt- |
| 24 | 796.5 | 64.1 | 276 | 21 | AA658207 | Canine flt-3 ligand |
| 25 | 791.5 | 63.7 | 265 | 21 | AA658211 | Feline mature flt- |
| 26 | 768.5 | 61.9 | 231 | 16 | AA67540 | Mouse flt-3 ligand |
| 27 | 768.5 | 61.9 | 231 | 20 | AA67768 | Murine flt-3 ligand |
| 28 | 768.5 | 61.9 | 231 | 22 | AA620186 | Mouse flt-3 ligand |
| 29 | 768.5 | 61.8 | 232 | 16 | AA66177 | Mouse flt-3 ligand |
| 30 | 764 | 61.5 | 232 | 22 | AA620189 | Mouse flt-3 ligand |
| 31 | 745 | 60.0 | 150 | 19 | AA677930 | Human flt-3 receptor |
| 32 | 745 | 60.0 | 150 | 19 | AA679054 | Human flt-3 receptor |
| 33 | 740.5 | 59.6 | 377 | 19 | AA678124 | Chimeric receptor |
| 34 | 739 | 59.5 | 143 | 19 | AA677926 | Human flt-3 receptor |
| 35 | 739 | 59.5 | 143 | 19 | AA679050 | Human flt-3 receptor |
| 36 | 737.5 | 59.4 | 349 | 19 | AA683289 | Human flt-3 ligand |
| 37 | 737.5 | 59.4 | 349 | 19 | AA678005 | Human flt-3 ligand |
| 38 | 736.5 | 59.3 | 340 | 19 | AA683291 | Human flt-3 ligand |
| 39 | 736.5 | 59.3 | 349 | 19 | AA683286 | Human flt-3 ligand |
| 40 | 736.5 | 59.3 | 349 | 19 | AA678008 | Human flt-3 ligand |
| 41 | 735 | 59.2 | 140 | 19 | AA677911 | Human flt-3 ligand |
| 42 | 735 | 59.2 | 140 | 19 | AA679035 | Human flt-3 receptor |
| 43 | 735 | 59.2 | 144 | 19 | AA677928 | Human flt-3 receptor |
| 44 | 735 | 59.2 | 144 | 19 | AA679052 | Human flt-3 receptor |
| 45 | 735 | 59.2 | 313 | 19 | AA683294 | Human flt-3 ligand |

ALIGNMENTS

| | | |
|----------|---------------------|--|
| RESULT 1 | AA67541 | standard; Protein: 235 AA. |
| ID | AA67541 | |
| XX | AA67541 | |
| AC | 05-AUG-1995 | (first entry) |
| XX | | |
| DE | Human flt-3 ligand. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| FT | Key | Location/Qualifiers |
| FT | Peptide | 1..26 |
| FT | | /label= Sig.peptide |
| FT | | /note= "signal peptide may extend to position 27" |
| FT | Domain | 27..182 |
| FT | | /label= Extracellular domain |
| FT | | /note= "extracellular domain may start at position 28" |
| FT | Domain | 183..205 |
| FT | | /label= Transmembrane domain |
| FT | Domain | 206..235 |
| FT | | /label= Cytoplasmic domain |
| PN | EP627487-A. | |
| PD | 07-DEC-1994. | |
| XX | | |
| PF | 19-MAY-1994. | 94EP-0303575. |
| XX | | |

PR 24-MAY-1993; 93US-0068394.
 PR 12-AUG-1993; 93US-0106463.
 PR 25-AUG-1993; 93US-0111758.
 PR 03-DEC-1993; 93US-0162407.
 PR 07-MAR-1994; 94US-0209502.
 PR 11-MAY-1994; 94US-0243545.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Beckmann MP, Lyman SD;
 XX
 DR WPI: 1995-008071/02.
 DR N-PSDB; AAO79079.
 XX
 PT Isolated ligands for flt 3 receptors - useful for treating
 PT anemia, AIDS and various cancers
 XX
 PS Disclosure: Page 29-30; 33pp; English.
 PS
 CC A human T-cell lambda-ct10 random primed cDNA library was
 CC screened with a fragment corresponding to the extracellular
 CC domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AAO79076)
 CC to isolate human flt3-L cDNA. Flt-3 stimulates progenitor and
 CC stem cells, and can be used e.g. in gene therapy protocols.
 XX
 SQ Sequence 235 AA;
 Query Match 100.0%; Score 1242; DB 16; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVALPAMSPPTYYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTV 60
 DB 1 MTVALPAMSPPTYYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTV 60
 QY 61 ASNLODEELCGGLMRVLVAQRMERLKTVAAGSKMOGLERVTETIHFYTKCAFOPPPSCL 120
 DB 61 ASNLODEELCGGLMRVLVAQRMERLKTVAAGSKMOGLERVTETIHFYTKCAFOPPPSCL 120
 QY 121 REVQNTISRLQETSEQVALKPMWTRNFSKLELQCPDPSSTLPMPSPRPLEATAPT 180
 DB 121 REVQNTISRLQETSEQVALKPMWTRNFSKLELQCPDPSSTLPMPSPRPLEATAPT 180
 QY 181 APQPLLLLLLPVGLLLAAAMCLHMORTRRTRPRGBOVPPVSPDILLVEH 235
 DB 181 APQPLLLLLLPVGLLLAAAMCLHMORTRRTRPRGBOVPPVSPDILLVEH 235
 RESULT 2
 AAM67769 standard; Protein: 235 AA.
 ID AAM67769;
 XX
 AC AAM67769;
 XX
 DT 25-MAR-1999 (first entry)
 XX
 DE Human flt3-ligand.
 XX
 KW Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L;
 KW immunogenic; autoimmune disease; organ transplantation; food allergy;
 KW tissue transplantation.
 XX
 OS Homo sapiens.
 OS
 PN WO9857655-A1.
 XX
 PD 23-DEC-1998.
 XX
 PF 12-JUN-1998; 98WO-US12085.
 XX
 PR 17-JUN-1997; 97US-0877421.
 XX
 PA (IMMV) IMMUNEX CORP.

XX
 PI Abbott NM, Nowat AM, Viney JL;
 XX
 DR WPI: 1999-070422/06.
 DR N-PSDB; AAV81506.
 XX
 PT Methods for initiating or enhancing antigen specific immune
 PT tolerance - by using murine or human flt3 ligand
 XX
 PS Claim 1; Page 14-15; 25pp; English.
 PS
 CC A method has been developed of initiating or enhancing: (i) an antigen-
 CC specific immune tolerance; or (ii) immunotolerance of a therapeutic
 CC immunogenic molecule by addition of a polypeptide, before, after or with
 CC the mucosal administration of an immunotolerizing amount of the antigen
 CC or therapeutic molecule, respectively. The polypeptide is capable of
 CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3
 CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino
 CC acids 28-y of human flt3-L, where y is an amino acid between 160-235;
 CC and c) a polypeptide that has at least 90% identity to the polypeptides
 CC of either (a) or (b). The method ameliorates the effects of autoimmune
 CC diseases, food allergies or organ or tissue rejection following
 CC transplantation. Administration of flt3-L allows lower doses of antigens
 CC to be used in vivo for mucosally administered antigens. The present
 CC sequence represents human flt3-L.
 XX
 SQ Sequence 235 AA;
 Query Match 100.0%; Score 1242; DB 20; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVALPAMSPPTYYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTV 60
 DB 1 MTVALPAMSPPTYYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTV 60
 QY 61 ASNLODEELCGGLMRVLVAQRMERLKTVAAGSKMOGLERVTETIHFYTKCAFOPPPSCL 120
 DB 61 ASNLODEELCGGLMRVLVAQRMERLKTVAAGSKMOGLERVTETIHFYTKCAFOPPPSCL 120
 QY 121 REVQNTISRLQETSEQVALKPMWTRNFSKLELQCPDPSSTLPMPSPRPLEATAPT 180
 DB 121 REVQNTISRLQETSEQVALKPMWTRNFSKLELQCPDPSSTLPMPSPRPLEATAPT 180
 QY 181 APQPLLLLLLPVGLLLAAAMCLHMORTRRTRPRGBOVPPVSPDILLVEH 235
 DB 181 APQPLLLLLLPVGLLLAAAMCLHMORTRRTRPRGBOVPPVSPDILLVEH 235
 RESULT 3
 AAY69719 standard; Protein: 235 AA.
 ID AAY69719;
 XX
 AC AAY69719;
 XX
 DT 05-JUL-2000 (first entry)
 XX
 DE Full length wild type human flt-3 protein.
 XX
 KW Immunomodulator; immunosuppressive; cytostatic; antineoplastic; anti-HIV;
 KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia.
 XX
 OS Homo sapiens.
 OS
 PN WO200001823-A2.
 XX
 PD 13-JAN-2000.
 XX

PF 25-JUN-1999; 99WO-US14296.
 XX
 PR 02-JUL-1998; 98US-0109100.
 XX
 PA (IMMUNEX CORP.
 XX
 PI Graddis TJ, McGrew JT;
 XX
 DR WPI: 2000-182115/16.
 XX
 N-PSDB: AA259064.
 XX
 PS
 Claim 1: Page 72-73; 90pp; English.

The invention relates to novel soluble flt-3 ligand (flt-3-L) polypeptides which exhibit increased or decreased biological activity relative to the full length wild type (this sequence) or mature (AA69720) flt-3-L polypeptides. The flt-3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt-3-L protein can be used to induce cellular expansion (especially in vivo) or differentiation, e.g. in the hematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, small cell lung, testicular or ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute leukemia.

Sequence 235 AA:

Query Match 100.0%; Score 1242; DB 21; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MVLAPAMSPPTTYLLLLLSGLSGTOPCSFQHSPTSSDFAVKIRELSYLDYDPVY 60
 DB 1 MVLAPAMSPPTTYLLLLLSGLSGTOPCSFQHSPTSSDFAVKIRELSYLDYDPVY 60
 OY 61 ASNLQDEELCGGLMRLVLAQRMMERLKTAVAGSKMGLERVNTIEHFVTKCAFPSPSC 120
 DB 61 ASNLQDEELCGGLMRLVLAQRMMERLKTAVAGSKMGLERVNTIEHFVTKCAFPSPSC 120
 OY 121 RPYQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPSPSRLLEATAPT 180
 DB 121 RPYQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPSPSRLLEATAPT 180
 OY 181 APOPLLLLLLPVGLLLAAMCLHMORTRRTPRGQVPPVPSPOLLVENH 235
 DB 181 APOPLLLLLLPVGLLLAAMCLHMORTRRTPRGQVPPVPSPOLLVENH 235

RESULT 4

AAAB20192

ID AAB20192 standard; Protein: 235 AA.

AAAB20192;

14-MAY-2001 (first entry)

Human flt-3 ligand.

XX flt-3 ligand; fms-like tyrosine kinase; human; vaccinia;
 KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;
 KM lymphoma; autoimmune disease; infection; gene therapy
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 FT Peptide 1..26
 FT /label= Signal_peptide
 FT Protein 27..235
 FT /label= Mature_protein
 FT Domain 27..182
 FT /label= Extracellular_domain
 FT Domain 183..205
 FT /label= Transmembrane_domain
 FT Domain 206..235
 FT /label= Cytoplasmic_domain

WO200109303-A2.

08-FEB-2001.

31-JUL-2000; 2000WO-US20679.

30-JUL-1999; 99US-0146170.

(VICA-) VICAL INC.

Hermanson GG;

WPI: 2001-123319/13.

N-PSDB: AAF30310.

Immunogenic compositions comprising flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis) -

Claim 2: Page 132-133; 149pp; English.

The present sequence is that of human fms-like tyrosine kinase (flt-3 ligand). The invention is directed to enhancing the immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a flt-3 ligand-encoding polynucleotide, and 1 or more antigen- or cytokine-encoding polynucleotides. The flt-3 ligand-encoding polynucleotide may encode the present full-length human flt-3 ligand polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185, or 27-235 of the ligand. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of flt-3 ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of: (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections; (b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs. Various other examples of these diseases are given in the specification.

Sequence 235 AA:

Query Match 100.0%; Score 1242; DB 22; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MVLAPAMSPPTTYLLLLLSGLSGTOPCSFQHSPTSSDFAVKIRELSYLDYDPVY 60
 DB 1 MVLAPAMSPPTTYLLLLLSGLSGTOPCSFQHSPTSSDFAVKIRELSYLDYDPVY 60
 OY 61 ASNLQDEELCGGLMRLVLAQRMMERLKTAVAGSKMGLERVNTIEHFVTKCAFPSPSC 120
 DB 61 ASNLQDEELCGGLMRLVLAQRMMERLKTAVAGSKMGLERVNTIEHFVTKCAFPSPSC 120
 OY 121 RPYQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPSPSRLLEATAPT 180
 DB 121 RPYQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPSPSRLLEATAPT 180

Db 121 RFGVNTISRLDQETSEQLVAKPWITRONSRLCLQCPDSSSTLPMPSPRLTAAPT 180

QY 181 APQPLLILLLLPVGLLLAAAMCLHMORTRRRTPRPGQVPVPSP@LLLVEN 235

Db 181 APQPLLILLLLPVGLLLAAAMCLHMORTRRRTPRPGQVPVPSP@LLLVEN 235

RESULT 5

ABB08129 ID ABB08129 standard; protein: 235 AA.

AC ABB08129; 10-SEP-2002 (first entry)

XX Human Flt3L polypeptide.

XX De Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;

XX Km fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;

XX Km tuberculostatic; cyostatic; human; Flt3L.

XX OS Homo sapiens.

XX PN WO200236141-A2.

XX PD 10-MAY-2002.

XX PF 30-OCT-2001; 2001WO-US44834.

XX PR 02-NOV-2000; 2000US-245721P.

XX PA (IMMEX) IMMEX CORP.

XX PI Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE

XX P1 Thomas EK;

XX DR WPI: 2002-500114/53.

XX PT Treating an individual suffering from infection, e.g. inflammation,

XX PT chickenpox or AIDS, by administering a combination of dendritic cell

XX PT mobilization factor or maturation agent; T cell enhancing factor and

XX PT antigen-specific T cells -

PS Disclosure: Page 37-38; 43pp; English.

XX CC The invention relates to treating an individual at risk for or suffering

XX CC from infection with a pathogenic or opportunistic organism. The method

XX CC involves administering a combination of two to five agents comprising:

XX CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation

XX CC agent; (c) dendritic cell activation agent; (d) T-cell enhancing factor;

XX CC or (e) activated, antigen-specific T cells. The methods are useful for

XX CC treating an individual at risk for or suffering from infection with a

XX CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria

XX CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.

XX CC T. cruzi), which causes Chagas' disease. The methods are especially

XX CC useful for treating an individual suffering from immunosuppression by

XX CC enhancing a lymphocyte-mediated immune response. In particular, the

XX CC method is useful for treating inflammations, chickenpox, oral or genital

XX CC herpes, mononucleosis, multilocal leukoencephalopathy, hepatitis, AIDS,

XX CC T cell leukemia or T cell lymphoma. The activated antigen-presenting

XX CC dendritic cells are useful as a vaccine adjuvant. The present sequence

XX CC represents a human Flt3L polypeptide fragment, that can be used as a

XX CC dendritic cell mobilisation factor.

XX Sequence 235 AA:

Query Match 100.0%; Score 1242; DB 23; Length 235;

Best Local Similarity 100.0%; Pred. No. 5e-109;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPPTVYLLLLSSGSLGTDCSFQHSPISSDPAVKIRLSDVLLQDYPTV 60

Db 1 MTVLAPAWSPPTVYLLLLSSGSLGTDCSFQHSPISSDPAVKIRLSDVLLQDYPTV 60

QY 61 ASNLODEELGGLMRLVLAQRMERIKTVAGSKMGLLERVNTETHEFVTKCAFQPPSCL 120

Db 61 ASNLODEELGGLMRLVLAQRMERIKTVAGSKMGLLERVNTETHEFVTKCAFQPPSCL 120

QY 121 RFGVNTISRLDQETSEQLVAKPWITRONSRLCLQCPDSSSTLPMPSPRLTAAPT 180

Db 121 RFGVNTISRLDQETSEQLVAKPWITRONSRLCLQCPDSSSTLPMPSPRLTAAPT 180

QY 181 APQPLLILLLLPVGLLLAAAMCLHMORTRRRTPRPGQVPVPSP@LLLVEN 235

Db 181 APQPLLILLLLPVGLLLAAAMCLHMORTRRRTPRPGQVPVPSP@LLLVEN 235

RESULT 6

AAR6175 ID AAR6175 standard; peptide: 235 AA.

AC AAR6175; 10-AUG-1995 (first entry)

XX Human S86/S109 Flt3 ligand peptide sequence.

XX DE Flt3 ligand; tyrosine kinase receptor ligand.

XX OS Homo sapiens.

XX PN WO9426891-A.

XX PD 24-NOV-1994.

XX PF 18-MAY-1994; 94WO-US05150.

XX PR 19-MAY-1993; 93US-0065231.

XX PR 07-JUL-1993; 93US-0089263.

XX PR 16-JUL-1993; 93US-0092549.

XX PR 13-AUG-1993; 93US-0106340.

XX PR 24-AUG-1993; 93US-0112391.

XX PR 19-NOV-1993; 93US-0151111.

XX PR 03-DEC-1993; 93US-0162413.

XX PA (INRM) INST NAT SANTE & RECH MEDICALE.

XX PA (SCHE) SCHERING CORP.

XX PI Birnbaum D, Cuipepper JA, Hannum CH, Lee FD;

XX P1 N-PSDB; AAQ79642.

XX DR WPI: 1995-006787/01.

XX PT New ligand for the Flt3 tyrosine kinase receptor - and related

XX PT nucleic acid, vectors, host cells and antibodies, useful for

XX PT treating abnormal cell physiology and proliferation, e.g. cancer,

XX PT also for diagnosis and drug screening

PS Claim 11; Page 76-77; 90pp; English.

XX CC A cDNA library from the human stromal cell line 293SV48, in

XX CC pMT85, was screened with an 800 bp fragment derived from

XX CC mouse clone T118. This fragment encompasses the coding region

XX CC conserved between two mouse clones, T118 and T110. Approx. 20

XX CC positive clones were selected and partially sequenced. Two

XX CC clones, S86 and S109, were found to be approx. 75% homologous

XX CC to the mouse clones over the first 163 AAs. Clone S86 continued

XX CC to show homology to T110 until the stop codon, although to a

XX CC lesser degree, for an overall homology of 66%. Clones T118 and

XX CC S109 do not show homology to each other or to the other clones

XX CC after mouse residue 163 (human residue 160). An additional mouse

XX CC clone designated MB8 has a 29 AA insert at the junction between

XX CC the common and divergent portions of the mouse ligand.

XX Sequence 235 AA:

| Query | Seq | Score | DB | Length | 235: |
|-----------------------|---|---|-----------|-------------|------|
| Query Match | 99.5%; | Score 1236; | DB 22; | Length 235; | |
| Best Local Similarity | 99.6%; | Pred. No. 1.8e-108; | | | |
| Matches 234; | Conservative 0; | Mismatches 1; | Indels 0; | Gaps 0; | |
| QY | 1 | MTVLAPAPSPPTYYLLLLLLSSGSLSGTQDCSPHSPISDPFAVKIRELSDYLLQDPVNY | 60 | | |
| Db | 1 | MTVLAPAPSPPTYYLLLLLLSSGSLSGTQDCSPHSPISDPFAVKIRELSDYLLQDPVNY | 60 | | |
| QY | 61 | ASNLDDEELCGGLMRLVLAQRMRERLKTAVGSKMGGILLERVNTEIHFVTKACAFOPPSCL | 120 | | |
| Db | 61 | ASNLDDEELCGGLMRLVLAQRMRERLKTAVGSKMGGILLERVNTEIHFVTKACAFOPPSCL | 120 | | |
| QY | 121 | REVQGNISRLQETSEOLVALKPKWTRKQFNSCLFELQCCPDSSTLPRLPPSPRLPENTAPT | 180 | | |
| Db | 121 | REVQGNISRLQETSEOLVALKPKWTRKQFNSCLFELQCCPDSSTLPRLPPSPRLPENTAPT | 180 | | |
| QY | 181 | APQPLPLLLLLLPVLVLLLAAMCLHMORTRRRTPRPGQGVPPVPSPODLLVEH | 235 | | |
| Db | 181 | APQPLPLLLLLLPVLVLLLAAMCLHMORTRRRTPRPGQGVPPVPSPODLLVEH | 235 | | |
| RESULT 8 | | | | | |
| ID | AAV69721 | standard; Protein; 212 AA. | | | |
| XX | AAV69721; | | | | |
| XX | 05-JUL-2000 (first entry) | | | | |
| DT | Human flt-3 mutein L-3H. | | | | |
| DE | | | | | |
| XX | Immunomodulator; immunosuppressive; cytosolic; antianemic; anti-HIV; | | | | |
| KW | neuroprotective; antiallergic; flt3 ligand; flt3-l; wild type; allergy; | | | | |
| KW | cell surface tyrosine kinase receptor; hematopoietic progenitor cell; | | | | |
| KW | cellular expansion; cellular differentiation; natural killer cell; | | | | |
| KW | cancer; dendritic cell; immune response; autoimmunity; immunosuppression; | | | | |
| KW | myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma; | | | | |
| KW | multiple myeloma; leukemia; muteln. | | | | |
| XX | | | | | |
| OS | Homo sapiens. | | | | |
| OS | Synthetic. | | | | |
| XX | WO200001823-A2. | | | | |
| PN | 13-JAN-2000. | | | | |
| PD | 25-JUN-1999; | 99WO-US14296. | | | |
| XX | 02-JUL-1998; | 98US-0109100. | | | |
| XX | | | | | |

| Query Match | Best Local Similarity | Matches | Conservative | Mismatches | Indels | Gaps |
|--|--|---------------|--------------|------------|--------|------|
| 89.7%; Score 1114; DB 19; Length 209; | 100.0%; Pred. No. 5.1e-97; | 209; | 0; | 0; | 0; | 0; |
| 27 TDQCSFGHSPSSDPFAVKIRELSLDYLDQVYVAASNLODELCGGMLRYLAQRMRRL 86 | 1 TDQCSFGHSPSSDPFAVKIRELSLDYLDQVYVAASNLODELCGGMLRYLAQRMRRL 86 | | | | | |
| 87 KTVAGSKMOGLLERNTNFIHVTKCAFPQPSCLRFQVNTNLSRLQETSSEGLVALKPKPT 146 | 61 KTVAGSKMOGLLERNTNFIHVTKCAFPQPSCLRFQVNTNLSRLQETSSEGLVALKPKPT 120 | | | | | |
| 147 RQNSRRCLELCCQPDSSSLPPWBSRPLEATAPAPQPPDLLLPLLVGLLLAAAMCLH 206 | 121 RQNSRRCLELCCQPDSSSLPPWBSRPLEATAPAPQPPDLLLPLLVGLLLAAAMCLH 180 | | | | | |
| 207 WQTRRRRTPRPGEQVPPVPSQDILLVEH 235 | 181 WQTRRRRTPRPGEQVPPVPSQDILLVEH 209 | | | | | |
| RESULT 10 | AAI69720 | | | | | |
| ID | AAI69720 | standard; | Protein: | 209 | AA. | |
| XX | AAI69720; | | | | | |
| XX | AC | | | | | |
| DT | 05-JUL-2000 | (first entry) | | | | |
| DE | Mature wild type human flt-3 protein. | | | | | |
| XX | | | | | | |

KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia.
 KW
 OS Homo sapiens.
 XX
 XX WO200001823-A2.
 XX
 XX 13-JAN-2000.
 XX
 XX 25-JUN-1999; 99WO-US14296.
 XX
 XX 02-JUL-1998; 98US-0109100.
 XX
 XX (IMMV) IMMUNEX CORP.
 XX
 XX Graddis TJ, McGrew JT;
 XX
 XX WPI: 2000-182115/16.
 XX
 XX N-PSDB; AAZ59064.
 XX
 PS Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122
 XX
 PS Claim 1; Page 89-90; 90pp; English.
 XX
 XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAV69719) or mature (this sequence) flt3-L
 CC polypeptides. The flt3-L protein binds cell surface tyrosine kinase
 CC receptors and regulate growth and differentiation of hematopoietic
 CC progenitor cells. The flt3-L protein can be used to induce cellular
 CC expansion (especially in vivo) or differentiation, e.g. in
 CC hematopoietic, natural killer (NK) or dendritic cells, especially in the
 CC presence of growth factors such as interleukins, colony stimulating
 CC factors or protein kinases. The protein can also modulate, augment, or
 CC enhance a patient's immune response and can be used to treat an immune
 CC disorder (e.g. allergy, autoimmunity or immunosuppression). The protein
 CC may be used to treat a pathological condition e.g. myelodysplasia,
 CC aplastic anemia, HIV infection, breast, small cell lung, testicular or
 CC ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
 CC leukemia.
 CC
 XX Sequence 209 AA:
 SQ
 Query Match 89.7%; Score 1114; DB 21; Length 209;
 Best Local Similarity 100.0%; Pred. No. 5; 1e-97;
 Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 27 TODCSFQHSPISSDFAVKIRELSYDLLODYPYVASNLODEFLCGGLMWLAQRMNERL 95
 DB 1 TODCSFQHSPISSDFAVKIRELSYDLLODYPYVASNLODEFLCGGLMWLAQRMNERL 50
 OY 87 KTVAGSKMOGLLEERYNTEIHFTKCAFOPPSCLEFVOTNISRLLOETSEQLVAKPMT 146
 DB 61 KTVAGSKMOGLLEERYNTEIHFTKCAFOPPSCLEFVOTNISRLLOETSEQLVAKPMT 120
 OY 147 RQNFSCRLELOCOPDSSITLPPWSPRPLEATAPAPOPPLDLLLLPVGULLLAAMCJH 206
 DB 121 RQNFSCRLELOCOPDSSITLPPWSPRPLEATAPAPOPPLDLLLLPVGULLLAAMCJH 180
 OY 207 WQTRRRTPRGEQVPPVPSPODLLLVEH 235
 DB 181 WQTRRRTPRGEQVPPVPSPODLLLVEH 209
 RESULT 11
 AAY69723

ID AAY69723 standard; Protein: 209 AA.
 XX
 AC AAY69723;
 XX
 DT 05-JUL-2000 (first entry)
 XX
 DE Human flt-3 mutein K84E.
 XX
 KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutein.
 KW
 OS Homo sapiens.
 XX
 XX Synthetic.
 XX
 XX WO200001823-A2.
 XX
 XX 13-JAN-2000.
 XX
 XX 25-JUN-1999; 99WO-US14296.
 XX
 XX 02-JUL-1998; 98US-0109100.
 XX
 XX (IMMV) IMMUNEX CORP.
 XX
 XX Graddis TJ, McGrew JT;
 XX
 XX WPI: 2000-182115/16.
 XX
 XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122
 XX
 PS Claim 4; Page 84-85; 90pp; English.
 XX
 XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel, flt-3
 CC ligands and comprises the K84E mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
 CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.
 CC
 XX Sequence 209 AA:
 SQ
 Query Match 89.4%; Score 1110; DB 21; Length 209;
 Best Local Similarity 99.5%; Pred. No. 1; 2e-96;
 Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 27 TODCSFQHSPISSDFAVKIRELSYDLLODYPYVASNLODEFLCGGLMWLAQRMNERL 86
 DB 1 TODCSFQHSPISSDFAVKIRELSYDLLODYPYVASNLODEFLCGGLMWLAQRMNERL 60
 OY 87 KTVAGSKMOGLLEERYNTEIHFTKCAFOPPSCLEFVOTNISRLLOETSEQLVAKPMT 146
 DB 61 KTVAGSKMOGLLEERYNTEIHFTKCAFOPPSCLEFVOTNISRLLOETSEQLVAKPMT 120
 OY 147 RQNFSCRLELOCOPDSSITLPPWSPRPLEATAPAPOPPLDLLLLPVGULLLAAMCJH 206
 DB 121 RQNFSCRLELOCOPDSSITLPPWSPRPLEATAPAPOPPLDLLLLPVGULLLAAMCJH 180
 OY 207 WQTRRRTPRGEQVPPVPSPODLLLVEH 235
 DB 181 WQTRRRTPRGEQVPPVPSPODLLLVEH 209
 RESULT 11
 AAY69723

Db 121 RNF5RCLLELCQOPDSSSTLPSPSPRLPPLATAPAPOPPLLLLLPVGILLAAACLH 180

QY 207 WQTRRRTPRPGEOVPVPSPDOLLVEH 235

Db 181 WQTRRRTPRPGEOVPVPSPDOLLVEH 209

RESULT 12

AAV69726 standard; Protein: 209 AA.

AAV69726:

05-JUL-2000 (first entry)

Human flt-3 mutein Q122R.

Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma; multiple myeloma; leukemia; mutein.

Homo sapiens.

Synthetic.

MO200001823-A2.

13-JAN-2000.

25-JUN-1999; 99MO-US14296.

02-JUL-1998; 98US-0109100.

(IMMV) IMMUNEX CORP.

Graddis TJ, McGrew JT;

WPI: 2000-182115/16.

Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological conditions

PT contains amino acid substitutions at positions 8, 84, 118 or 122

Claim 4; Page 88-89; 90pp; English.

The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAV69719) or mature (AAV69720) flt3-L polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the Q122R mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, small cell lung, testicular or ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute leukemia.

Sequence 209 AA:

Query Match 89.4%; Score 1110; DB 21; Length 209;

Best Local Similarity 99.5%; Pred. No. 1.2e-96;

Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

27 TDGSPGHSPISSDFAVKIRELSDYLLQDYPVTVAASNLODELCGGLMRLVLAQRMMERL 86

Db 1 TDGSPGHSPISSDFAVKIRELSDYLLQDYPVTVAASNLODELCGGLMRLVLAQRMMERL 60

QY 87 KTVAGSKMOGLLEAVNEIHFVTKCAFCQPPSCRFQVOTNISRLQETSEOLVALKMIT 146

Db 61 KTVAGSKMOGLLEAVNEIHFVTKCAFCQPPSCRFQVOTNISRLQETSEOLVALKMIT 120

QY 147 RNF5RCLLELCQOPDSSSTLPSPSPRLPPLATAPAPOPPLLLLLPVGILLAAACLH 206

Db 121 RNF5RCLLELCQOPDSSSTLPSPSPRLPPLATAPAPOPPLLLLLPVGILLAAACLH 180

QY 207 WQTRRRTPRPGEOVPVPSPDOLLVEH 235

Db 181 WQTRRRTPRPGEOVPVPSPDOLLVEH 209

RESULT 13

AAV69727 standard; Protein: 209 AA.

AAV69727:

05-JUL-2000 (first entry)

Human flt-3 mutein L26F.

Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma; multiple myeloma; leukemia; mutein.

Homo sapiens.

Synthetic.

MO200001823-A2.

13-JAN-2000.

25-JUN-1999; 99MO-US14296.

02-JUL-1998; 98US-0109100.

(IMMV) IMMUNEX CORP.

Graddis TJ, McGrew JT;

WPI: 2000-182115/16.

Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological conditions

PT contains amino acid substitutions at positions 8, 84, 118 or 122

Claim 13; Page 82-83; 90pp; English.

The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAV69719) or mature (AAV69720) flt3-L polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the L26F mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, small cell lung, testicular or ovarian cancer, lymphoma, multiple

CC myeloma, neuroblastoma or acute leukemia.
XX Sequence 209 AA;
Query Match 89.4%; Score 1110; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 1.2e-96;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLDYLDYPTVASNLODEELCGGLMRLVLAQRMWERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLDYLDYPTVASNLODEELCGGLMRLVLAQRMWERL 60

QY 87 KTVAGSKMOGLIERVNTIEHFVTKCAFOPPSCLEFVOTNISRLQETSEQLVALKPWIT 146
DB 61 KTVAGSKMOGLIERVNTIEHFVTKCAFOPPSCLEFVOTNISRLQETSEQLVALKPWIT 120

QY 147 RQNSRCLELQCCPDSSSTLPPWSPRPLEATPTAPQPPDLLLLLPVGLLLAAACI 206
DB 121 RQNSRCLELQCCPDSSSTLPPWSPRPLEATPTAPQPPDLLLLLPVGLLLAAACI 180

QY 207 WQTRRRTPRGEQVPPVSPQDLLLVEH 235
DB 181 WQTRRRTPRGEQVPPVSPQDLLLVEH 209

RESULT 14
AAV69729 standard; Protein: 209 AA.
XX AAV69729;
AC AAV69729;
XX 05-JUL-2000 (first entry)
DT 05-JUL-2000 (first entry)
DE Human flt-3 mutleln A64T.
XX

KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutleln.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200001823-A2.
PN 13-JAN-2000.
XX
XX 25-JUN-1999; 99WO-US14296.
PF 25-JUN-1999; 99WO-US14296.
XX
XX 02-JUL-1998; 98US-0109100.
PR 02-JUL-1998; 98US-0109100.
XX
XX (IMMV) IMMUNEX CORP.
PA
XX Graddis TJ, McGrew JT;
PI
XX WPI: 2000-182115/16.
DR
XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
PT contains amino acid substitutions at positions 8, 84, 118 or 122
XX
XX Claim 13; Page 78-79; 90pp; English.
PS
XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L.
CC polypeptides. This sequence represents an example of the novel flt3
CC ligands and comprises the L26F mutant polypeptide. The flt3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can

CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX
XX Sequence 209 AA;
SQ Sequence 209 AA;
Query Match 89.4%; Score 1110; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 1.2e-96;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLDYLDYPTVASNLODEELCGGLMRLVLAQRMWERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLDYLDYPTVASNLODEELCGGLMRLVLAQRMWERL 60

QY 87 KTVAGSKMOGLIERVNTIEHFVTKCAFOPPSCLEFVOTNISRLQETSEQLVALKPWIT 146
DB 61 KTVAGSKMOGLIERVNTIEHFVTKCAFOPPSCLEFVOTNISRLQETSEQLVALKPWIT 120

QY 147 RQNSRCLELQCCPDSSSTLPPWSPRPLEATPTAPQPPDLLLLLPVGLLLAAACI 206
DB 121 RQNSRCLELQCCPDSSSTLPPWSPRPLEATPTAPQPPDLLLLLPVGLLLAAACI 180

QY 207 WQTRRRTPRGEQVPPVSPQDLLLVEH 235
DB 181 WQTRRRTPRGEQVPPVSPQDLLLVEH 209

RESULT 15
AAV69722 standard; Protein: 209 AA.
XX AAV69722;
AC AAV69722;
XX 05-JUL-2000 (first entry)
DT 05-JUL-2000 (first entry)
DE Human flt-3 mutleln H8Y.
XX

KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutleln.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200001823-A2.
PN 13-JAN-2000.
XX
XX 25-JUN-1999; 99WO-US14296.
PF 25-JUN-1999; 99WO-US14296.
XX
XX 02-JUL-1998; 98US-0109100.
PR 02-JUL-1998; 98US-0109100.
XX
XX (IMMV) IMMUNEX CORP.
PA
XX Graddis TJ, McGrew JT;
PI
XX WPI: 2000-182115/16.
DR
XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
PT contains amino acid substitutions at positions 8, 84, 118 or 122
XX

PS Claim 4; Page 81-82; 90pp; English.

XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibit increased or decreased biological activity relative to
 CC the full length wild type (AA69719) or mature (AA69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt-3
 CC ligands and comprises the H81 mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
 CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.
 XX
 SQ Sequence 209 AA;

Query Match

Best Local Similarity 89.2%; Score 1108; DB 21; Length 209;

Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 27 TODCSFQHSPISSDPAVKIRELSDYLLQDYPVIVASNLQDELCGLRLVLAQRWHERL 86
 DB 1 TODCSFYSPISDPAVKIRELSDYLLQDYPVIVASNLQDELCGLRLVLAQRWHERL 60
 OY 87 KYVAGSKMOGLLEVRNFIHFVTKCAFQPPSCIREYQINISRLQETSEQLVALKEWIT 146
 DB 61 KYVAGSKMOGLLEVRNFIHFVTKCAFQPPSCIREYQINISRLQETSEQLVALKEWIT 120
 OY 147 RQNFRCLELQCCQDSSSTLPPWSPRLPEATAPQPLLLLELPVGLCLAAACGLH 206
 DB 121 RQNFRCLELQCCQDSSSTLPPWSPRLPEATAPQPLLLLELPVGLLLAANGLH 180
 OY 207 WQTRRRTPRRGEQVPPVPSFODLLVEH 235
 DB 181 WQTRRRTPRRGEQVPPVPSFODLLVEH 209

Search completed: May 27, 2003, 18:27:13
 Job time : 37 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 27, 2003, 18:26:36 ; Search time 15 Seconds
(without alignments)
460.959 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242
Sequence: 1 MVLAPAWSPFTYLLLL...RPGQVPPVSPDLLVEH 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued_Patents_AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/Backfilltest.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 1242 | 100.0 | 235 | 1 | US-08-243-545-6 |
| 2 | 1242 | 100.0 | 235 | 2 | US-08-993-962-6 |
| 3 | 1242 | 100.0 | 235 | 4 | US-09-150-841-6 |
| 4 | 1242 | 100.0 | 235 | 5 | US-09-109-100-1 |
| 5 | 1242 | 100.0 | 235 | 5 | PCT-US94-05365-6 |
| 6 | 1124 | 90.5 | 212 | 4 | US-09-109-100-10 |
| 7 | 1114 | 89.7 | 209 | 4 | US-09-109-100-18 |
| 8 | 1110 | 89.4 | 209 | 4 | US-09-109-100-9 |
| 9 | 1110 | 89.4 | 209 | 4 | US-09-109-100-12 |
| 10 | 1110 | 89.4 | 209 | 4 | US-09-109-100-14 |
| 11 | 1110 | 89.4 | 209 | 4 | US-09-109-100-17 |
| 12 | 1108 | 89.2 | 209 | 4 | US-09-109-100-11 |
| 13 | 1108 | 89.2 | 209 | 4 | US-09-109-100-15 |
| 14 | 1107 | 89.1 | 209 | 4 | US-09-109-100-13 |
| 15 | 1106 | 89.0 | 209 | 4 | US-09-109-100-8 |
| 16 | 1100 | 88.6 | 209 | 4 | US-09-109-100-16 |
| 17 | 768.5 | 61.9 | 231 | 1 | US-08-243-545-2 |
| 18 | 768.5 | 61.9 | 231 | 2 | US-08-993-962-2 |
| 19 | 768.5 | 61.9 | 231 | 4 | US-09-160-841-2 |
| 20 | 768.5 | 61.9 | 231 | 5 | PCT-US94-05365-2 |
| 21 | 765.5 | 61.6 | 231 | 1 | US-08-220-3798-7 |
| 22 | 765.5 | 61.6 | 231 | 5 | PCT-US95-03866-6 |
| 23 | 506.5 | 40.8 | 137 | 4 | US-09-109-100-15 |
| 24 | 154 | 12.4 | 42 | 5 | PCT-US94-05150-17 |
| 25 | 91.5 | 7.4 | 675 | 1 | US-08-317-522A-5 |
| 26 | 91.5 | 7.4 | 675 | 1 | US-08-439-818A-9 |
| 27 | 91.5 | 7.4 | 675 | 2 | US-08-751-965-9 |

| | | | | | | |
|----|------|-----|-----|---|-------------------|--------------------|
| 28 | 91.5 | 7.4 | 675 | 2 | US-08-738-975-9 | Sequence 9, Appl1 |
| 29 | 91.5 | 7.4 | 675 | 2 | US-08-728-626-9 | Sequence 9, Appl1 |
| 30 | 91.5 | 7.4 | 675 | 2 | US-08-808-559A-9 | Sequence 9, Appl1 |
| 31 | 87.5 | 7.0 | 415 | 4 | US-09-006-353A-6 | Sequence 6, Appl1 |
| 32 | 87.5 | 7.0 | 415 | 4 | US-09-573-966-6 | Sequence 6, Appl1 |
| 33 | 85 | 6.8 | 366 | 1 | US-08-004-492-8 | Sequence 8, Appl1 |
| 34 | 84.5 | 6.8 | 913 | 3 | US-08-445-640-4 | Sequence 4, Appl1 |
| 35 | 84.5 | 6.8 | 913 | 3 | US-08-170-558-4 | Sequence 4, Appl1 |
| 36 | 84.5 | 6.8 | 913 | 3 | US-08-447-314-4 | Sequence 4, Appl1 |
| 37 | 84.5 | 6.8 | 913 | 3 | US-08-445-451-4 | Sequence 4, Appl1 |
| 38 | 84 | 6.8 | 107 | 4 | US-09-220-528-52 | Sequence 52, Appl1 |
| 39 | 84 | 6.8 | 220 | 4 | US-09-220-528-26 | Sequence 26, Appl1 |
| 40 | 83.5 | 6.7 | 429 | 1 | US-07-964-589-2 | Sequence 2, Appl1 |
| 41 | 83.5 | 6.7 | 429 | 5 | PCT-US93-02024-2 | Sequence 2, Appl1 |
| 42 | 83.5 | 6.7 | 671 | 3 | US-09-121-321-16 | Sequence 16, Appl1 |
| 43 | 83.5 | 6.7 | 671 | 4 | US-08-933-803A-16 | Sequence 16, Appl1 |
| 44 | 83 | 6.7 | 28 | 5 | PCT-US94-05150-12 | Sequence 12, Appl1 |
| 45 | 83 | 6.7 | 758 | 1 | US-07-756-250-16 | Sequence 16, Appl1 |

ALIGNMENTS

RESULT 1
US-08-243-545-6
Sequence 6, Application US/08243545
Patent No. 5554512
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,545
FILING DATE: 11-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-243-545-6

Query Match 100.0%; Score 1242; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSVLLQDYPTV 60
DB 1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSVLLQDYPTV 60
QY 61 ASNLODELGGLMRVLVAQRMERLKTAVGSKMKGILLERNTIHFVTKCAFQPPPSCL 120
DB 61 ASNLODELGGLMRVLVAQRMERLKTAVGSKMKGILLERNTIHFVTKCAFQPPPSCL 120
QY 121 RFVQTNISRLQETSEQVLVAKPWITRONFSRCLELQCPDSSSTLPPWSPRPLEATAPT 180
DB 121 RFVQTNISRLQETSEQVLVAKPWITRONFSRCLELQCPDSSSTLPPWSPRPLEATAPT 180
QY 181 APQPPLLLLLLPVGLLLAAACLHWQRTRRTPRPEGVPPVPSQDILLVH 235
DB 181 APQPPLLLLLLPVGLLLAAACLHWQRTRRTPRPEGVPPVPSQDILLVH 235

RESULT 2

US-08-993-962-6
Sequence 6, Application US/08993962
Patent No. 5843423

GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,962
FILING DATE: December 18, 1993

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-993-962-6

Query Match 100.0%; Score 1242; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSVLLQDYPTV 60
DB 1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSVLLQDYPTV 60
QY 61 ASNLODELGGLMRVLVAQRMERLKTAVGSKMKGILLERNTIHFVTKCAFQPPPSCL 120
DB 61 ASNLODELGGLMRVLVAQRMERLKTAVGSKMKGILLERNTIHFVTKCAFQPPPSCL 120
QY 121 RFVQTNISRLQETSEQVLVAKPWITRONFSRCLELQCPDSSSTLPPWSPRPLEATAPT 180
DB 121 RFVQTNISRLQETSEQVLVAKPWITRONFSRCLELQCPDSSSTLPPWSPRPLEATAPT 180
QY 181 APQPPLLLLLLPVGLLLAAACLHWQRTRRTPRPEGVPPVPSQDILLVH 235
DB 181 APQPPLLLLLLPVGLLLAAACLHWQRTRRTPRPEGVPPVPSQDILLVH 235

RESULT 3

US-09-160-841-6
Sequence 6, Application US/09160841
Patent No. 6190655

GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,841
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-160-841-6

Query Match 100.0%; Score 1242; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTYYLLLLLLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
DB 1 MTVLAPAMSPPTYYLLLLLLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
QY 61 ASNQDELGGLMRLVLAQRMMERLKTVAAGSKMOGLLERNTETIHFTKCAFOPPPSCL 120
DB 61 ASNQDELGGLMRLVLAQRMMERLKTVAAGSKMOGLLERNTETIHFTKCAFOPPPSCL 120
QY 121 RFVOTNISRLQETSEQLVALKPIWTRONFSRCLELOCOPDSSSTLPWMSRPLEATAPT 180
DB 121 RFVOTNISRLQETSEQLVALKPIWTRONFSRCLELOCOPDSSSTLPWMSRPLEATAPT 180
QY 181 APOPPPLLLLLLPVGLLLLAAMCLHMQRTRRRTPRGEQVPVPSPQDILLVH 235
DB 181 APOPPPLLLLLLPVGLLLLAAMCLHMQRTRRRTPRGEQVPVPSPQDILLVH 235

RESULT 4
US-09-109-100-1
Sequence 1, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109.100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-1

Query Match 100.0%; Score 1242; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTYYLLLLLLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
DB 1 MTVLAPAMSPPTYYLLLLLLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
QY 61 ASNQDELGGLMRLVLAQRMMERLKTVAAGSKMOGLLERNTETIHFTKCAFOPPPSCL 120
DB 61 ASNQDELGGLMRLVLAQRMMERLKTVAAGSKMOGLLERNTETIHFTKCAFOPPPSCL 120
QY 121 RFVOTNISRLQETSEQLVALKPIWTRONFSRCLELOCOPDSSSTLPWMSRPLEATAPT 180
DB 121 RFVOTNISRLQETSEQLVALKPIWTRONFSRCLELOCOPDSSSTLPWMSRPLEATAPT 180
QY 181 APOPPPLLLLLLPVGLLLLAAMCLHMQRTRRRTPRGEQVPVPSPQDILLVH 235
DB 181 APOPPPLLLLLLPVGLLLLAAMCLHMQRTRRRTPRGEQVPVPSPQDILLVH 235

RESULT 5
PCT-US94-05365-6
Sequence 6, Application PC/TUS9405365
GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for FLT3/FLK-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05365
FILING DATE: May 24, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: -to be assigned-
FILING DATE: May 11, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,502
FILING DATE: March 7, 1994
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,407
FILING DATE: December 3, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-05365-6

Query Match 100.0%; Score 1242; DB 5; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTYYLLLLLLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
DB 1 MTVLAPAMSPPTYYLLLLLLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
QY 61 ASNQDELGGLMRLVLAQRMMERLKTVAAGSKMOGLLERNTETIHFTKCAFOPPPSCL 120
DB 61 ASNQDELGGLMRLVLAQRMMERLKTVAAGSKMOGLLERNTETIHFTKCAFOPPPSCL 120
QY 121 RFVOTNISRLQETSEQLVALKPIWTRONFSRCLELOCOPDSSSTLPWMSRPLEATAPT 180

Db 121 RFQVOTISRLLQETSEQLVAKPMITRONFSRCLQCCPDSSSTLPSPRPLEATAPMT 180
OY 181 APOPELLLLLVGLLLAAAMCLHMQTRRRRTPRGEOVPVPSPDILLVEH 235
Db 181 APOPELLLLLVGLLLAAAMCLHMQTRRRRTPRGEOVPVPSPDILLVEH 235

RESULT 6

US-09-109-100-10
; Sequence 10, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Gradadis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-10

Query Match 90.5%; Score 1124; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.2e-105;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 SCQDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLMRVLVAQRMERL 84
Db 2 SCQDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLMRVLVAQRMERL 61
OY 85 RKTAVGSKMOGLLERVNTIEHFVTKCAFQPPSCRFVQTNISRLLQETSEQLVAKPM 144
Db 62 RKTAVGSKMOGLLERVNTIEHFVTKCAFQPPSCRFVQTNISRLLQETSEQLVAKPM 121
OY 145 ITRONFSRCLQCCPDSSSTLPSPRPLEATAPAPPELLLLLVGLLLAAAMC 204
Db 122 ITRONFSRCLQCCPDSSSTLPSPRPLEATAPAPPELLLLLVGLLLAAAMC 181
OY 205 LHMQRTRRRTPRGEVPPVPSPDILLVEH 235
Db 182 LHMQRTRRRTPRGEVPPVPSPDILLVEH 212

RESULT 7

US-09-109-100-18
; Sequence 18, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Gradadis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-18

Query Match 89.7%; Score 1114; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.2e-104;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLMRVLVAQRMERL 86
Db 181 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLMRVLVAQRMERL 86

Db 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLMRVLVAQRMERL 60
OY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCRFVQTNISRLLQETSEQLVAKPMIT 146
Db 61 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCRFVQTNISRLLQETSEQLVAKPMIT 120
OY 147 RQNFSCRLEQCCPDSSSTLPSPRPLEATAPAPPELLLLLVGLLLAAAMC 206
Db 121 RQNFSCRLEQCCPDSSSTLPSPRPLEATAPAPPELLLLLVGLLLAAAMC 180
OY 207 WQTRRRTPRGEVPPVPSPDILLVEH 235
Db 181 WQTRRRTPRGEVPPVPSPDILLVEH 209

RESULT 8

US-09-109-100-9
; Sequence 9, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Gradadis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-9

Query Match 89.4%; Score 1110; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 3e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLMRVLVAQRMERL 86
Db 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLMRVLVAQRMERL 60
OY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCRFVQTNISRLLQETSEQLVAKPMIT 146
Db 61 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCRFVQTNISRLLQETSEQLVAKPMIT 120
OY 147 RQNFSCRLEQCCPDSSSTLPSPRPLEATAPAPPELLLLLVGLLLAAAMC 206
Db 121 RQNFSCRLEQCCPDSSSTLPSPRPLEATAPAPPELLLLLVGLLLAAAMC 180
OY 207 WQTRRRTPRGEVPPVPSPDILLVEH 235
Db 181 WQTRRRTPRGEVPPVPSPDILLVEH 209

RESULT 9

US-09-109-100-12
; Sequence 12, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Gradadis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-12

Query Match 89.4%; Score 1110; DB 4; Length 209;
 Best Local Similarity 99.5%; Pred. No. 3e-104;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFOHSPISDFAVKIRELSYLDYDYPVTVASNL0DEELCGGLMRLVLAQRMERL 86
 Db 1 TODCSFOHSPISDFAVKIRELSYLDYDYPVTVASNL0DEELCGGLMRLVLAQRMERL 60
 QY 87 KTVAGSKMOGLLEVRNTEIHFVTKCAFOPPSCLEFVQTNISRLLOETSEQLVALKPWIT 146
 Db 61 KTVAGSKMOGLLEVRNTEIHFVTKCAFOPPSCLEFVQTNISRLLOETSEQLVALKPWIT 120
 QY 147 R0NFSRCLLEOCOPDSSSTLPPWSPRPLEATAPAP0PPLLILLPVGILLAAACMLH 206
 Db 121 R0NFSRCLLEOCOPDSSSTLPPWSPRPLEATAPAP0PPLLILLPVGILLAAACMLH 180
 QY 207 W0TRRRTPRGEQVPPVPSPODLLVEH 235
 Db 181 W0TRRRTPRGEQVPPVPSPODLLVEH 209

RESULT 10

US-09-109-100-14
 ; Sequence 14, Application US/09109100C
 ; Patent No. 6291661
 ; GENERAL INFORMATION:
 ; APPLICANT: Graddis, Thomas J.
 ; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
 ; FILE REFERENCE: 03260.0028
 ; CURRENT APPLICATION NUMBER: US/09/109,100C
 ; CURRENT FILING DATE: 1998-07-02
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Patentln Ver. 2.1
 ; SEQ ID NO 14
 ; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-109-100-14

Query Match 89.4%; Score 1110; DB 4; Length 209;
 Best Local Similarity 99.5%; Pred. No. 3e-104;
 Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFOHSPISDFAVKIRELSYLDYDYPVTVASNL0DEELCGGLMRLVLAQRMERL 86
 Db 1 TODCSFOHSPISDFAVKIRELSYLDYDYPVTVASNL0DEELCGGLMRLVLAQRMERL 60
 QY 87 KTVAGSKMOGLLEVRNTEIHFVTKCAFOPPSCLEFVQTNISRLLOETSEQLVALKPWIT 146
 Db 61 KTVAGSKMOGLLEVRNTEIHFVTKCAFOPPSCLEFVQTNISRLLOETSEQLVALKPWIT 120
 QY 147 R0NFSRCLLEOCOPDSSSTLPPWSPRPLEATAPAP0PPLLILLPVGILLAAACMLH 206
 Db 121 R0NFSRCLLEOCOPDSSSTLPPWSPRPLEATAPAP0PPLLILLPVGILLAAACMLH 180
 QY 207 W0TRRRTPRGEQVPPVPSPODLLVEH 235
 Db 181 W0TRRRTPRGEQVPPVPSPODLLVEH 209

RESULT 11

US-09-109-100-17
 ; Sequence 17, Application US/09109100C
 ; Patent No. 6291661
 ; GENERAL INFORMATION:
 ; APPLICANT: Graddis, Thomas J.
 ; APPLICANT: McGrew, Jeffrey T.
 ; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
 ; FILE REFERENCE: 03260.0028
 ; CURRENT APPLICATION NUMBER: US/09/109,100C
 ; CURRENT FILING DATE: 1998-07-02

; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Patentln Ver. 2.1
 ; SEQ ID NO 17
 ; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-109-100-17

Query Match 89.4%; Score 1110; DB 4; Length 209;
 Best Local Similarity 99.5%; Pred. No. 3e-104;
 Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFOHSPISDFAVKIRELSYLDYDYPVTVASNL0DEELCGGLMRLVLAQRMERL 86
 Db 1 TODCSFOHSPISDFAVKIRELSYLDYDYPVTVASNL0DEELCGGLMRLVLAQRMERL 60
 QY 87 KTVAGSKMOGLLEVRNTEIHFVTKCAFOPPSCLEFVQTNISRLLOETSEQLVALKPWIT 146
 Db 61 KTVAGSKMOGLLEVRNTEIHFVTKCAFOPPSCLEFVQTNISRLLOETSEQLVALKPWIT 120
 QY 147 R0NFSRCLLEOCOPDSSSTLPPWSPRPLEATAPAP0PPLLILLPVGILLAAACMLH 206
 Db 121 R0NFSRCLLEOCOPDSSSTLPPWSPRPLEATAPAP0PPLLILLPVGILLAAACMLH 180
 QY 207 W0TRRRTPRGEQVPPVPSPODLLVEH 235
 Db 181 W0TRRRTPRGEQVPPVPSPODLLVEH 209

RESULT 12

US-09-109-100-11
 ; Sequence 11, Application US/09109100C
 ; Patent No. 6291661
 ; GENERAL INFORMATION:
 ; APPLICANT: Graddis, Thomas J.
 ; APPLICANT: McGrew, Jeffrey T.
 ; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
 ; FILE REFERENCE: 03260.0028
 ; CURRENT APPLICATION NUMBER: US/09/109,100C
 ; CURRENT FILING DATE: 1998-07-02
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Patentln Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-109-100-11

Query Match 89.2%; Score 1108; DB 4; Length 209;
 Best Local Similarity 99.5%; Pred. No. 4.8e-104;
 Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFOHSPISDFAVKIRELSYLDYDYPVTVASNL0DEELCGGLMRLVLAQRMERL 86
 Db 1 TODCSFOHSPISDFAVKIRELSYLDYDYPVTVASNL0DEELCGGLMRLVLAQRMERL 60
 QY 87 KTVAGSKMOGLLEVRNTEIHFVTKCAFOPPSCLEFVQTNISRLLOETSEQLVALKPWIT 146
 Db 61 KTVAGSKMOGLLEVRNTEIHFVTKCAFOPPSCLEFVQTNISRLLOETSEQLVALKPWIT 120
 QY 147 R0NFSRCLLEOCOPDSSSTLPPWSPRPLEATAPAP0PPLLILLPVGILLAAACMLH 206
 Db 121 R0NFSRCLLEOCOPDSSSTLPPWSPRPLEATAPAP0PPLLILLPVGILLAAACMLH 180
 QY 207 W0TRRRTPRGEQVPPVPSPODLLVEH 235
 Db 181 W0TRRRTPRGEQVPPVPSPODLLVEH 209

RESULT 13

US-09-109-100-15
 ; Sequence 15, Application US/09109100C
 ; Patent No. 6291661

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: GENERAL INFORMATION:
: APPLICANT: Graddis, Thomas J.
: APPLICANT: McGrew, Jeffrey T.
: TITLE OF INVENTION: ERT3-1 MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03260.0028
: CURRENT APPLICATION NUMBER: US/09/109.100C
: CURRENT FILING DATE: 1998-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 15
: LENGTH: 209
: TYPE: prt
: ORGANISM: Homo sapiens
: US-09-109-100-15

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| | | | | |
|---------------------------|--------|---------------------|-----------|-------------|
| Query Match | 89.28; | Score 1108; | DB 4; | Length 209; |
| Best Local Similarity | 99.58; | Pred. No. 4.8e-104; | | |
| Matches 208; Conservative | 0; | Mismatches 1; | Indels 0; | Gaps 0; |

| | | | | | |
|----|-----|----------------------|----------------------|-----------------------|-----|
| QY | 27 | TQDCSFQHSPLTSSPFAVKI | IRELSYDYLQDQVYVAASNQ | ODEELCGGMRLVLAQRMWRL | 86 |
| Db | 1 | TQDCSFQHSPLTSSDPAVKI | IRELSYDYLQDQVYVAASNQ | ODEELCGGMRLVLAQRMWRL | 60 |
| QY | 87 | KTVAGSKMOGLLERVNEI | HFVTKCAFQPPSCIRFVQ | TNISRLQETSSEQVALKPMIT | 146 |
| Db | 61 | KTVAGSKMOGLLERVNEI | HFVTKCAFQPPSCIRFVQ | TNISRLQETSSEQVALKPMIT | 120 |
| QY | 147 | RQNSRSCLELOCQPDSS | TLPPPMSPRPLEAATPAQ | PPILLLLLVGLLLAAAMC | 206 |
| Db | 121 | RQNSRSCLELOCQPDSS | TLPPPMSPRPLEAATPAQ | PPILLLLLVGLLLAAAMC | 180 |
| QY | 207 | WQTRRRRTPRGEOVPP | VPVPSQODLLVEH | 235 | |
| Db | 181 | WQTRRRRTPRGEOVPP | VPVPSQODLLVEH | 209 | |

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RESULT 14
US-09-109-100-13
: Sequence 13, Application US/09109100C
: Patent No. 6291661
:
: GENERAL INFORMATION:
:
: APPLICANT: Graddis, Thomas J.
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03360, 0028
: CURRENT APPLICATION NUMBER: US/09/109,100C
: CURRENT FILING DATE: 1998-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Patentin Ver. 2.1
:
: SEQ ID NO 13
:
: LENGTH: 209
:
: TYPE: PRT
: ORGANISM: Homo sapiens
:
: US-09-109-100-13

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| | | | | |
|---------------------------|--------|-------------------|-----------|-------------|
| Query Match | 89.1% | Score 1107; | DB 4; | Length 209; |
| Best Local Similarity | 99.5%; | Pred. No. 6e-104; | | |
| Matches 208; Conservative | 0; | Mismatches 1; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|---|-----|
| QY | 27 | TODSFOHSPISSPFAVKIRELSYLLQDVVTAASNLQDEELCGLMRLVLAQRMERL | 86 |
| Db | 1 | TODSFOHSPISSPFAVKIRELSYLLQDQPVVTAASNLQDEELCGLMRLVLAQRMERL | 60 |
| QY | 87 | KTVAGSKMOGLLEFERNMEIHFVTKCAQPPESCRLFVQTNISRLQETSQDLVAKPWT | 146 |
| Db | 61 | KTVAGSKMOGLLEFERNMEIHFVTKCAQPPESCRLFVQTNISRLQETSQDLVAKPWT | 120 |
| QY | 147 | RQNSRCLCIELCCOPDSSITLPPWMSPRPLEATAPAPQPELILLLLLEVGLLAAACGLH | 206 |
| Db | 121 | RQNSRCLCIELCCOPDSSITLPPWMSPRPLEATAPAPQPELILLLLLEVGLLAAACGLH | 180 |
| QY | 207 | WQTRRRRTPRGGEQVPPVPSQDILLVEH | 235 |
| Db | | | |

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Db      181  MORTRRRTPRGEOVPPVSPDOLLVHEH 209

      RESULT 15
      US-09-109-100-8
      ; Sequence 8, Application US/09109100C
      ; Patent No. 6291661
      ; GENERAL INFORMATION:
      ; APPLICANT: Graddiss, Thomas J.
      ; APPLICANT: McGrew, Jeffrey T.
      ; TITLE OF INVENTION: FLT3-I- MUTANTS AND METHODS OF USE
      ; FILE REFERENCE: 03260, 0028
      ; CURRENT APPLICATION NUMBER: US/09/109,100C
      ; CURRENT FILING DATE: 1998-07-02
      ; NUMBER OF SEQ. ID NOS: 20
      ; SOFTWARE: Patentln Ver. 2.1
      ; SEQ ID NO 8
      ; LENGTH: 209
      ; TYPE: prt
      ; ORGANISM: Homo sapiens
      ; US-09-109-100-8

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| | | | | |
|-----------------------|-----------------|---------------------|-----------|-------------|
| Query Match | 89.0%; | Score 1106; | DB 4; | Length 209; |
| Best Local Similarity | 99.5%; | Pred. No. 7.6e-104; | | |
| Matches 208; | Conservative 0; | Mismatches 1; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|--|-----|
| Oy | 87 | KTVAGSKMOGLLERVNEIHFVTKCAFQPPPSCLREPVQTNISRLLOETSEQVALKFWIT | 146 |
| Db | 61 | KTVAGSKMOGLLERVNEIHFVTKCAFQPPPSCLREPVQTNISRLLOETSEQVALKFWIT | 120 |
| Oy | 147 | RQNSRCLLELOCQDPSSITLPPPMSPRPLEARAPARQPPILLLLLLVGILLLLLAAACLH | 206 |
| Db | 121 | RQNSRCLLELOCQDPSSITLPPPMSPRPLEARAPARQPPILLLLLLVGILLLLLAAACLH | 180 |
| Oy | 207 | WQTRRRRTPRPEOVPPVPSPQDILLVEH | 235 |
| Db | 181 | WQTRRRRTPRPEOVPPVPSPQDILLVEH | 209 |

Search completed: May 27, 2003, 18:28:59
Job time : 17 secs

Dd 121 RFVNTNISHLLDPTSSQTLAKPKWITRRNFSGCLTELOCQDPSSLTVPBPSGALTEATLP 160

Qy 181 APQP-LLLLLLEVGILLIAAACLM-QTRRTTRPGEQVPVS-----PD 229
||| | ||||||| ||:: ||||| : |||: ||| || 1:1
Db 181 AQAQRLLIIIVALLIMSTACLMRRRRRRSYPGQRLTARSESHLPED 236

RESULT 2

Q9M209 PRELIMINARY. PBT. 301 AA
ID Q9M219

| | EMBL | EMBL | EMBL |
|------------|---|---|------|
| AC | 06MAY-2000 | (T-EMBLrel. 15, Created) | |
| DT | 01-OCT-2000 | (T-EMBLrel. 15, Last sequence update) | |
| DT | 01-OCT-2000 | (T-EMBLrel. 15, Last sequence update) | |
| DT | 01-JUN-2002 | (T-EMBLrel. 21, Last annotation update) | |
| DE | Flt3 ligand | | |
| OS | Felis silvestris catus (Cat). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis. | | |
| NCBI_TaxId | 9685; | | |

SQ SEQUENCE 291 AA; 32459 MW; 8F85A10A5EA0DCC6 CRC64;

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|---|--------|----|-------|-----|------|----|------|-----|----|----|-----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|
| QY | 1 | MTVLPA | PN | ASPTT | YLL | LLLL | LL | SSGL | STQ | DC | SC | QHS | P | IS | SD | FA | VK | I | EL | S | D | Y | L | L | O | D | P | V | Y | 60 |
| | | 1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | LL | |
| | | 1 | | MTVL | PA | NSPT | S | LL | LL | LL | | | | | | | | | | | | | | | | | | | | |

RESULT 3

09GKED
DDI TWENTY.
DDE.
203

| ID | ORGANO | PREFILMNAME | PRG | 252 AA |
|------------------|--|---|-----|--------|
| AC | ORGREO | | | |
| DT | 01-MAR-2001 | (TREMBLrel. 16, Created) | | |
| DT | 01-MAR-2001 | (TREMBLrel. 16, Last sequence update) | | |
| DT | 01-DEC-2001 | (TREMBLrel. 19, Last annotation update) | | |
| DE | Flt3 ligand isoform-1. | | | |
| OS | Bos taurus (Bovine). | | | |
| OC | Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; | | | |
| OC | Bovidae; Bovinae; Bos. | | | |
| NCBI_TaxID=9913; | | | | |
| XX | | | | |

RL J. Immunol. 165:6966-6974(2000).
DR EMBL; AF282985; AAF93932.1; -.
DR InterPro; IPR004213; Flt3_L1g.
DR Pfam; PF02947; Flt3_L1g; 1.
SQ SEQUENCE 292 AA; 32330 MW; D68B9ED79221202D CRC64

| Query Match | Score | DB | Length |
|-------------|-------|----|--------|
| 67.68; | 840; | 6; | 292; |

| | | | |
|----|-----|---|-----|
| OY | 1 | MTVLAPAWSPPT-YLILLLLSGLSGTODCSFOHSPISSDPAVKIRELSDTYLLDYPVT | 59 |
| | | | |
| Db | 1 | MTVLAPAWSPPTSLLELLLELPGLGTPDCSFKHSPISSIFAIKTIKRLSKTYLLDYPVT | 60 |
| OY | 60 | VASINODELCGGIMRWLVLAORWMERIKTVAGASKMOGLEEVNTEIHFFVTKCAFOPPSC | 119 |
| | | : : : : : : | |
| Dd | 61 | VASNLDQDKICGATRRVLYLAORWRGRKLTAVAGSMKKLEDVNTIEHFVTSKAFOPLPSC | 120 |
| OY | 120 | LRFVOTNISRLLOETSEDLVALKPWITRONSRLCQLQCOPDSSTLRPPWSPRELEATP | 179 |
| | | : : : : : : | |
| Dd | 121 | LRFVANISHLLDPHQDEALKPWITHRNFSRLCEQLQCOPDSSTLLRPSPGALGATSL | 180 |
| OY | 180 | TAPDP-----LLLLLLPRGULLLAANCLMHQRTRRRTRPPREG | 220 |
| | | | |
| Dd | 181 | PGPSPLLELLLELLLPVALLIILLATACLCWMRRRRRTTRPREG | 224 |

RESULT 4

| | |
|--------|--------------|
| Q8WNW1 | |
| ID | Q8WNW1 |
| | PRELIMINARY; |
| | PRT; |
| | 292 AA |

AC Q8WNMI; 01-MAR-2002 (TREMblrefl. 20, Created)
 DT 01-MAR-2002 (TREMblrefl. 20, Last sequence update)
 DT 01-JUN-2002 (TREMblrefl. 21, Last annotation update)
 DE Flt3 ligand.
 GN FLT3 LIGAND.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hikoito H., Momtani E.;
 RT "Cloning of a cDNA for bovine flt3 ligand."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB051841; BAB76534.1; -
 DR InterPro; IPR004213; FLT3_L19.
 PLam; PF02947; flt3_119.1.
 SO SEQUENCE 292 AA; 3238 MW; 2A797E0C1199C1D9 CRC64;

| | | | | |
|---------------------------|--------|--------------------|-----------|-------------|
| Query Match | 67.2%; | Score 835; | DB 6; | Length 292; |
| Best Local Similarity | 75.9%; | Pred. NO. 3.2e-74; | | |
| Matches 170; Conservative | 12; | Mismatches 38; | Indels 4; | Gaps 2 |

| | | | | |
|----|-----|--|--|----|
| QY | 1 | MTVLAPAWSPPT | -YLLLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPVT | 59 |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| Db | 1 | MVVLAPAWSPPT | SLLLLLLLPGLGTPDCSFRRHSPISSFAFKIKLSKYLLODYPVT | 60 |
| QY | 60 | VASNIQDELCGGIMRLVLAQRMWERLKYTAAGSGMOGLLERNVETHEIFNFKCAFPORPSC | 119 | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| Db | 61 | VASNIQDOKLCGAWRVLVLAQRMGRRLKYTAAGSEMERLLEDVNETHEIFVNSCAFPOLPSC | 120 | |
| QY | 120 | LRFVQTNISRLQETSEQVLAKPMITRONFSRLCELEIQCPDSSSTLPMPSPPLRELTAP | 179 | |
| | | | | |
| | | | | |
| | | | | |
| Db | 121 | LRFVQTNISHLLODTHQGLERKRWITHRRNSRLCELEIQCPDPSSTLPMPSPCALATSL | 180 | |
| QY | 180 | TAPQPP--LILLLLIVGILLLAAMCLMQTRRRTPRQEG | 220 | |
| | | | | |
| | | | | |
| Db | 181 | PGQPSPLLLLLLLLIPVALLLATATACLCWRRRRRRTRTPGEC | 224 | |

RESULT 5

09G6D9
ID 09GKD9 PRELIMINARY; PRT; 274 AA.
AC 09GKD9
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Flt3 ligand isoform-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20570936; PubMed=11120823;
RA Mwangi W., Brown W.C., Palmer G.H.;
RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain
RT required for receptor binding and function using naturally occurring
RT ligand isoforms."
RL J. Immunol. 165:6966-6974(2000).
DR EMBL; AF282986; AAF9323.1; -
DR InterPro: IPR004213; Flt3_1lg.
DR Pfam: PF02947; flt3_1lg; 1.
SQ SEQUENCE 274 AA; 30372 MW; 725A7F7A95DA98B CRC64;
Query Match 60.1%; Score 746; DB 6; Length 274;
Best Local Similarity 69.6%; Pred. No. 1.8e-65;
Matches 156; Conservative 12; Mismatches 34; Indels 22; Gaps 3;
QY 1 MTVALPAMSP-IT-YLLLLLSGLSGTQDCSFQHSPISSPFAVKIRELSYLLQDYPT 59
DB 1 MTVALPAMSP-IT-YLLLLLSGLSGTQDCSFQHSPISSPFAVKIRELSYLLQDYPT 60
QY 60 VASNLQDEELCGGLMRVLVLAORWMEKLTAVGSKMKGLEEVNTEIHFTVCAROPPPSC 119
DB 61 VASNLQDEELCGGLMRVLVLAORWMEKLTAVGSKMKGLEEVNTEIHFTVCAROPPPSC 114
QY 120 LRFVQNTISRLQETSEQLVAKPWITR--QNFSCLELQCCOPDSSTLPPEWSPRELTAP 179
DB 115 -----QDTHQQLKALKPWITRNFSCLELQCCOPDSSTLPPEWSPRELTAP 162
QY 180 TAPQPP---LTLTLPLVGLLLLAANCLHWQTRRRRRPRGEG 220
DB 163 PGFSPILLLLLLLLPVALLLATAMCLCRWRRRRRRTRPYGER 206
RESULT 6
061104
ID 061104 PRELIMINARY; PRT; 172 AA.
AC 061104;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Flt3 ligand, T169 form.
GN Flt3L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K.,
RA Matsson J., Tsai S., Luh J., Guimares M.J., Mattei M.-G., Rosnet O.,
RA Blumberg P., Hannum C.;
RT "Flt3 ligand: expression, genomic organization, alternatively spliced
RT forms and processing."
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U44024; AAA93305.1; -
DR MGD; MGI:95560; Flt3L.
DR InterPro: IPR004213; Flt3_1lg.
DR InterPro: IPR001230; Prenyl_site.
DR Pfam: PF02947; flt3_1lg; 1.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.

SQ SEQUENCE 172 AA; 19465 MW; 04F0A01071E3384 CRC64;
Query Match 48.5%; Score 602.5; DB 11; Length 172;
Best Local Similarity 72.6%; Pred. No. 1.5e-51;
Matches 122; Conservative 15; Mismatches 28; Indels 3; Gaps 2;
QY 1 MTVALPAMSP-IT-YLLLLLSGLSGTQDCSFQHSPISSPFAVKIRELSYLLQDYPT 59
DB 1 MTVALPAMSP-IT-YLLLLLSGLSGTQDCSFQHSPISSPFAVKIRELSYLLQDYPT 60
QY 60 VASNLQDEELCGGLMRVLVLAORWMEKLTAVGSKMKGLEEVNTEIHFTVCAROPPPSC 119
DB 61 VASNLQDEELCGGLMRVLVLAORWMEKLTAVGSKMKGLEEVNTEIHFTVCAROPPPSC 120
QY 120 LRFVQNTISRLQETSEQLVAKPWITR--QNFSCLELQCCOPDSSTLPPEWSPRELTAP 165
DB 121 LRFVQNTISRLQETSEQLVAKPWITR--QNFSCLELQCCOPDSSTLPPEWSPRELTAP 168
RESULT 7
08VCH4
ID 08VCH4 PRELIMINARY; PRT; 169 AA.
AC 08VCH4;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to FMS-like tyrosine kinase 3 ligand.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue-Liver.
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019801; AAH19801.1; -
DR InterPro: IPR004213; Flt3_1lg.
DR Pfam: PF02947; flt3_1lg; 1.
KW Kinase.
SQ SEQUENCE 169 AA; 18986 MW; 5B4CA47D9724EFP2 CRC64;
Query Match 46.5%; Score 578; DB 11; Length 169;
Best Local Similarity 68.6%; Pred. No. 3.7e-49;
Matches 120; Conservative 14; Mismatches 29; Indels 12; Gaps 3;
QY 1 MTVALPAMSP-IT-YLLLLLSGLSGTQDCSFQHSPISSPFAVKIRELSYLLQDYPT 59
DB 1 MTVALPAMSP-IT-YLLLLLSGLSGTQDCSFQHSPISSPFAVKIRELSYLLQDYPT 60
QY 60 VASNLQDEELCGGLMRVLVLAORWMEKLTAVGSKMKGLEEVNTEIHFTVCAROPPPSC 119
DB 61 VASNLQDEELCGGLMRVLVLAORWMEKLTAVGSKMKGLEEVNTEIHFTVCAROPPPSC 120
QY 120 LRFVQNTISRLQETSEQLVAKPWITR--QNFSCLELQCCOPDSSTLPPEWSPRELTAP 172
DB 121 LRFVQNTISRLQETSEQLVAKPWITR--QNFSCLELQCCOPDSSTLPPEWSPRELTAP 166
RESULT 8
09LGC8
ID 09LGC8 PRELIMINARY; PRT; 579 AA.
AC 09LGC8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative extensin-like protein.
GN P0406H10.6 OR C01174.D05.5.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzae; Oryza.
OX NCBI_TaxID=4530;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RT clone: P0406H10."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
 RT clone: O01174_D05."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP002524; BAB07956.1; -
 DR EMBL: AP003118; BAB33013.1; -
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003592; LRR_out.
 DR InterPro: IPR002965; P_rich_extensn.
 DR Pfam: PF00560; LRR; 6.
 DR PRINTS: PRO1582; KV33CHANNEL.
 DR PRINTS: PRO1217; PRICHEXTENSN.
 DR SMART: SM00370; LRR; 5.
 DR PROSITE: PS00030; RRM_RNP_1; UNKNOWN_1.
 SQ SEQUENCE 579 AA; 62607 MW; 04457E18E7405AAF CRC64;

Query Match 9.1%; Score 112.5; DB 10; Length 579;
 Best local Similarity 23.7%; Pred. No. 0.013;
 Matches 54; Conservative 28; Mismatches 69; Indels 77; Gaps 11;

QY 17 LLLLSGLSGTDCSFQHSPISSDFAVKIRELSLDYLDQYPTVASNLQDEELCGGLMRL 76
 DB 244 ILIINIGL-----SCLPEVGM-LREIVTF-----DVSNRLAGPLPSA 282
 OY 77 VLAQRMMERLKTAVGSMOGLERVNTIEHFVTKCAFO-----PPPSCLRFV-----QT 125
 DB 283 VAGMKRYEQL-DVAHNILITAIPOAVCELPRLNFTFAVYFGEPPSCAHANPRYDDR 341
 QY 126 NI--SRLLQTSFQVLAALKWITRONFSR---CLELQCPDSSSTLPWPSPRLXATAP 179
 DB 342 NCLPNRPAQFTLRQCAAF-----FARPPVNCAMFQCKRFVAPALPPSPPPP--SPP 391
 QY 180 TAQPPPLLLLLPVGILLAAAMCLHMORTRRRTPRRGQVPPVSP 227
 DB 392 PSEPPP-----SPPSPSTSPPPP 411

RESULT 9
 QYGY11 PRELIMINARY; PRT; 668 AA.
 AC QYGY11;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Probable surface antigen p2.
 GN LM12.156.
 GN Leishmania major.
 OS Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OC NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
 RA Oliver K.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL390114; CAC02038.2; -
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001611; LRR.
 DR Pfam: PF00560; LRR; 6.
 DR PRINTS: PRO1217; PRICHEXTENSN.
 DR SMART: SM0181; EGF; 1.

SQ SEQUENCE 668 AA; 70725 MW; CEB3ECAABC490C94 CRC64;
 Query Match 8.4%; Score 104.5; DB 5; Length 668;
 Best local Similarity 26.6%; Pred. No. 0.093;
 Matches 63; Conservative 20; Mismatches 77; Indels 77; Gaps 13;

QY 4 LAPAWPTTYLLLLLSGLSGTDCSFQHSPISSDFAVKIRELSLDYLDQYPTVASN 63
 DB 149 LPPEWSSMPNLQTVRRLKLSGT-----LPADWS-SLKSLSNVLEDPIT----- 194
 OY 64 LDPEELCGGLMRVLVLAQRMMERLKTAVGSMOGLERVNTIEHFVTKCAFOPPP-----S 118
 DB 195 -----GL-----LPPEW-----GSLERIQQLVLRKILKGLRPLPPQSPMK 229
 QY 119 CLRFPVQ---TNISRLQ-----ETSEQLVALKP-WITRONFSRCLQLQCP 160
 DB 230 ALRFILTLDTGNTLSGTLPPQWSAMASVSLNLEGTVEVSGTLPPKWMISRL-QTLNLRRTK 288
 QY 161 DSSTLPPEWSPR-----PLEATAPTAPOP-----LLLLLLPVGLL--LLAAAM 203
 DB 289 VSGTLPEWSSMGSLANLQSLTVSGTLPPQWSMKKLTQLLTDTLLSGTLPAEM 345

RESULT 10
 QYGY33 PRELIMINARY; PRT; 648 AA.
 AC QYGY33;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Probable surface antigen p2.
 GN LM12.121.
 GN Leishmania major.
 OS Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OC NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
 RA Oliver K.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL390114; CAC02017.2; -
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR002965; P_rich_extensn.
 DR Pfam: PF00560; LRR; 7.
 DR PRINTS: PRO1217; PRICHEXTENSN.
 DR SMART: SM0181; EGF; 1.
 SQ SEQUENCE 648 AA; 68470 MW; 8EB78AC101E01286 CRC64;

Query Match 8.3%; Score 102.5; DB 5; Length 648;
 Best local Similarity 26.6%; Pred. No. 0.14;
 Matches 63; Conservative 20; Mismatches 77; Indels 77; Gaps 13;

QY 4 LAPAWPTTYLLLLLSGLSGTDCSFQHSPISSDFAVKIRELSLDYLDQYPTVASN 63
 DB 149 LPPEWSSMPNLVLAQRMERLKTAVGSMOGLERVNTIEHFVTKCAFOPPP-----S 118
 QY 195 -----GL-----LPPEW-----GSLERIQQLVLRKILKGLRPLPPQSPMK 229
 OY 119 CLRFPVQ---TNISRLQ-----ETSEQLVALKP-WITRONFSRCLQLQCP 160
 DB 230 ALRFILTLDTGNTLSGTLPPQWSAMASVSLNLEGTVEVSGTLPPKWMISRL-QTLNLRRTK 288
 QY 161 DSSTLPPEWSPR-----PLEATAPTAPOP-----LLLLLLPVGLL--LLAAAM 203
 DB 289 VSGTLPEWSSMGSLANLQSLTVSGTLPPQWSMKKLTQLLTDTLLSGTLPAEM 345

RESULT 11
 QYGY16 PRELIMINARY; PRT; 648 AA.

ID 2 Q8VIM6 PRELIMINARY; PRT: 1809 AA.
 AC Q8VIM6:
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Stereocilin.
 GN STRC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C;
 RX MEDLINE=21547528; PubMed=11687802;
 RA Verpy E., Masmondi S., Zwaenepoel I., Leibovici M., Hutchin T.P.,
 RA Del Castillo I., Nouaille S., Blanchard S., Laine S., Popot J.L.,
 RA Moreno F., Mueller R.F., Petit C.;
 RT "Mutations in a new gene encoding a protein of the hair bundle cause
 RT non-syndromic deafness at the DFNB16 locus."
 RL Nat. Genet. 29:345-349(2001).
 DR EMBL: AF375593; AAL35321.1; -
 DR MGD: MGI:2153816; Strc.
 SQ SEQUENCE 1809 AA; 196404 MW; 0123820980EC825 CRC64;
 Query Match 8.1%; Score 100.5; DB 11; Length 1809;
 Best Local Similarity 23.7%; Pred. No. 0.74;
 Matches 70; Conservative 25; Mismatches 93; Indels 107; Gaps 14;
 QY 3 VLAWMSFTYLL-----LLLL-----SSGLSGTDCSFQHSPISSDPAVKIRE 47
 DB 168 VLADWLPSTLMLLEGRFMALVOLQPSVDPNTATGIDG-----RE 208
 QY 48 LSDLLDLY--PVTVASNLQDEE-ICGSLMRLV---LAQRMERLKY----- 89
 DB 209 PAHFLOGGLGLTPAGELGSEALMGGLRTVGAFLYAAQEGELRTHSLQDEVESIM 268
 QY 90 -----AGSKMGLLERVNTETHEFTK-----AFQPPSCLRFVQTNISRL 131
 DB 269 GQPPDASGCGGNGNLLQQLLMGMRNLSMDARALGFLSGSPPPALLHCLSRGV--L 326
 QY 132 QETSEQLVAKPWITTRQNSFSCLELQCPDSDTLPP-----PMSPPLE 175
 DB 327 PRASQPAHISP---RQRALSVLEALCENHSQPEPPYSISNSIYLLCOHKIPATPRPP 383
 QY 176 AT---APTAPQPLLLLLLPVGLLLAAACLMQRTRRRPRGEOVP--PVPS 226
 DB 384 TTPRPPTTPPPPTTPTTPIP-----DTTQPPVTPRPPTTTPPPPS 426
 RESULT 12
 Q9N753 PRELIMINARY; PRT: 345 AA.
 AC Q9N753:
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Probable surface antigen p2.
 GN LM12.08.
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Bartell B.,
 RA Oliver K.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL390114; CAB98658.2; -
 DR InterPro: IPR001611; LRR
 DR InterPro: IPR003592; LRR_out.
 DR Pfam: Pf00560; LRR: 3.
 DR SMART: SM00370; LRR: 3.

SQ SEQUENCE 345 AA; 37530 MW; 06ECC850B1B54B70 CRC64;
 Query Match 7.9%; Score 98.5; DB 5; Length 345;
 Best Local Similarity 23.8%; Pred. No. 0.17;
 Matches 56; Conservative 21; Mismatches 57; Indels 101; Gaps 10;
 QY 6 PAWSFTYLLLLLSGLSGT-----QDCSFQHSPISSDPAVKIRELS 49
 DB 152 PEMWSMTLSVLNLNGTIGSTLPPQMGSKARSLQDQDGLSSLSMSAI----- 205
 QY 50 DYLLQDPVTVASNLQDEELG-----GLMRLVLAQRMERLKYAGSKMGLLERVTE 104
 DB 206 -----PMLASVSLKGNKFCGVCRTGRIRLVLL--WTSRTSTRAATA----- 245
 QY 105 IHFTKCAFQ--PPSCLRFYQTNISRLQETSEQLVALKPWITTRQNSFSCLELQCPD 161
 DB 246 --WLKRTQRPPLSPPPQRPRTSLT-----FPLRRQPR 278
 QY 162 SSTLPPSPPLLEATAPAPPLLL-----LLPVGLLLAAACLMQRTRR 212
 DB 279 LSRLPQALRRRLN-----PQPLRRRLNRPRLP-----QOTRR 313
 RESULT 13
 Q9DMH8 PRELIMINARY; PRT: 1240 AA.
 AC Q9DMH8:
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Pr2.
 GN R2.
 OS Rat cytomegalovirus (strain Mastricht).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC Betaherpesvirinae; Muromegalovirus.
 OX NCBI_TaxID=79700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MASTRICHT;
 RX MEDLINE=20366325; PubMed=10906222;
 RA Vink C., Beuken E., Bruggeman C.A.;
 RT "Complete DNA sequence of the rat cytomegalovirus genome."
 RL J. Virol. 74:7656-7665(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MASTRICHT;
 RX MEDLINE=20473137; PubMed=11018281;
 RA Gruijthuisen Y.K., Beuken E., Bruggeman C.A., Vink C.;
 RT "Rat cytomegalovirus R89 is a highly conserved gene which expresses a
 RT spliced transcript."
 RL Virus Res. 69:119-130(2000).
 DR EMBL: AF232689; AAF99111.1; -
 SQ SEQUENCE 1240 AA; 125612 MW; 33B6C13DC6A272B0 CRC64;
 Query Match 7.7%; Score 95.5; DB 12; Length 1240;
 Best Local Similarity 33.0%; Pred. No. 1.5;
 Matches 29; Conservative 8; Mismatches 18; Indels 33; Gaps 5;
 QY 160 PDSSTL-----PPWSPP--LEATAPAPQD-PLLLLLLPVGLLLAA 201
 DB 1060 PDSSTAVTGEATTERSTPATEPRPRPLPGVDALPLAQPITLLSLVPA----- 1112
 QY 202 AMCLHMORTRRTPRPGEOVPVPSPD 229
 DB 1113 -----OATRASPRPETDAP-PTPAD 1132
 RESULT 14
 Q9C5T0 PRELIMINARY; PRT: 658 AA.
 AC Q9C5T0:
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 27, 2003, 18:28:06 ; Search time 57 Seconds
(without alignments)
408.870 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242

Sequence: 1 MYVLAPAWSPTYLILLLL.....RPGEQVPPVPSQDLLLVEH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 375593 seqs, 99172665 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB pep:*

2: /cgn2_6/ptodata/2/pubppaa/PCF_NEW_PUB pep:*

3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB pep:*

4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB pep:*

5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB pep:*

6: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB pep:*

7: /cgn2_6/ptodata/2/pubppaa/PCFUS_PUBCOMB pep:*

8: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB pep:*

9: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB pep:*

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12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB pep:*

13: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB pep:*

14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|---------------------|--------------------|
| 1 | 1242 | 100.0 | 235 | 9 US-10-095-449-6 | Sequence 6, Appl1 |
| 2 | 1242 | 100.0 | 235 | 10 US-09-448-378-1 | Sequence 1, Appl1 |
| 3 | 1242 | 100.0 | 235 | 10 US-09-983-806-6 | Sequence 6, Appl1 |
| 4 | 1242 | 100.0 | 235 | 10 US-09-904-536-1 | Sequence 1, Appl1 |
| 5 | 1124 | 90.5 | 212 | 10 US-09-904-536-10 | Sequence 10, Appl1 |
| 6 | 1114 | 89.7 | 209 | 10 US-09-904-536-18 | Sequence 18, Appl1 |
| 7 | 1110 | 89.4 | 209 | 10 US-09-904-536-9 | Sequence 9, Appl1 |
| 8 | 1110 | 89.4 | 209 | 10 US-09-904-536-12 | Sequence 12, Appl1 |
| 9 | 1110 | 89.4 | 209 | 10 US-09-904-536-14 | Sequence 14, Appl1 |
| 10 | 1110 | 89.4 | 209 | 10 US-09-904-536-17 | Sequence 17, Appl1 |
| 11 | 1108 | 89.2 | 209 | 10 US-09-904-536-11 | Sequence 11, Appl1 |
| 12 | 1108 | 89.2 | 209 | 10 US-09-904-536-15 | Sequence 15, Appl1 |
| 13 | 1107 | 89.1 | 209 | 10 US-09-904-536-13 | Sequence 13, Appl1 |
| 14 | 1106 | 89.0 | 209 | 10 US-09-904-536-8 | Sequence 8, Appl1 |
| 15 | 1100 | 88.6 | 209 | 10 US-09-904-536-16 | Sequence 16, Appl1 |
| 16 | 822 | 66.2 | 156 | 9 US-10-053-355A-1 | Sequence 1, Appl1 |
| 17 | 768.5 | 61.9 | 231 | 9 US-10-095-449-2 | Sequence 2, Appl1 |
| 18 | 768.5 | 61.9 | 231 | 10 US-09-448-378-2 | Sequence 2, Appl1 |
| 19 | 768.5 | 61.9 | 231 | 10 US-09-983-806-2 | Sequence 2, Appl1 |

| | | | | | |
|----|-------|------|------|-----------------------|--------------------|
| 20 | 506.5 | 40.8 | 137 | 10 US-09-904-536-19 | Sequence 19, Appl1 |
| 21 | 91.5 | 7.4 | 674 | 10 US-09-899-471-2 | Sequence 2, Appl1 |
| 22 | 91.5 | 7.4 | 698 | 9 US-09-866-050A-509 | Sequence 509, App |
| 23 | 91.5 | 7.4 | 698 | 9 US-09-863-818A-8 | Sequence 8, Appl1 |
| 24 | 91.5 | 7.4 | 698 | 10 US-09-899-471-5 | Sequence 5, Appl1 |
| 25 | 89.5 | 7.2 | 874 | 10 US-09-826-508-26 | Sequence 26, Appl1 |
| 26 | 89.5 | 7.2 | 941 | 9 US-09-793-139-47 | Sequence 47, Appl1 |
| 27 | 89.5 | 7.2 | 941 | 9 US-10-300-616-31 | Sequence 31, Appl1 |
| 28 | 89.5 | 7.2 | 941 | 10 US-09-818-879-47 | Sequence 47, Appl1 |
| 29 | 89.5 | 7.2 | 941 | 10 US-09-211-755B-47 | Sequence 47, Appl1 |
| 30 | 88.5 | 7.1 | 1257 | 9 US-10-109-324-2 | Sequence 2, Appl1 |
| 31 | 88 | 7.1 | 238 | 9 US-10-174-363-30 | Sequence 30, Appl1 |
| 32 | 87.5 | 7.0 | 415 | 9 US-09-917-372-20 | Sequence 20, Appl1 |
| 33 | 87.5 | 7.0 | 415 | 10 US-09-826-512-6 | Sequence 6, Appl1 |
| 34 | 87.5 | 7.0 | 415 | 10 US-09-907-372-20 | Sequence 20, Appl1 |
| 35 | 87.5 | 7.0 | 415 | 10 US-09-935-727-8 | Sequence 8, Appl1 |
| 36 | 87.5 | 7.0 | 479 | 9 US-10-108-605-57 | Sequence 57, Appl1 |
| 37 | 87.5 | 7.0 | 570 | 9 US-09-991-496-104 | Sequence 104, App |
| 38 | 87.5 | 7.0 | 570 | 10 US-09-874-923-104 | Sequence 104, App |
| 39 | 85.5 | 6.9 | 519 | 10 US-09-925-300-1680 | Sequence 1680, App |
| 40 | 84.5 | 6.8 | 610 | 10 US-09-783-708-1 | Sequence 1, Appl1 |
| 41 | 84.5 | 6.8 | 913 | 10 US-09-223-490-4 | Sequence 4, Appl1 |
| 42 | 84.5 | 6.8 | 1134 | 9 US-10-001-873-50 | Sequence 50, Appl1 |
| 43 | 84 | 6.8 | 107 | 10 US-09-220-920-52 | Sequence 52, Appl1 |
| 44 | 84 | 6.8 | 220 | 9 US-10-001-054-56 | Sequence 56, Appl1 |
| 45 | 84 | 6.8 | 220 | 10 US-09-220-920-26 | Sequence 26, Appl1 |

ALIGNMENTS

RESULT 1
US-10-095-449-6
Sequence 6, Application US/10095449

Patent No. US20020160004A1

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.

Beckmann, M. Patricia

TITLE OF INVENTION: Ligands for Flt3/Flk-2 Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESSES:

ADDRESSSEE: Stephen L. Malaska, Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.0.1

SOFTWARE: Microsoft Word, Version #5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/095,449

FILING DATE: 13-Mar-2002

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/669,692

FILING DATE: 24-JUN-1996

APPLICATION NUMBER: US/08/162,407

FILING DATE: December 3, 1993

APPLICATION NUMBER: 08/111,758

FILING DATE: August 25, 1993

APPLICATION NUMBER: 08/106,463

FILING DATE: August 12, 1993

APPLICATION NUMBER: 08/068,394

FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 2813-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-095-449-6

Query Match 100.0%; Score 1242; DB 10; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFOHSPISDPFAVKIRELSYLLQDYVTV 60
DB 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFOHSPISDPFAVKIRELSYLLQDYVTV 60
QY 61 ASNLQDEELCGGLMRVLVLAORRMERLKTVAAGSKMOGLLEEVNTEIHFTKCAEQPPPSCL 120
DB 61 ASNLQDEELCGGLMRVLVLAORRMERLKTVAAGSKMOGLLEEVNTEIHFTKCAEQPPPSCL 120
QY 121 RFVQNTISRLLQETSEQVLAALKPWITRONFSRCLELOCOPDSSSTLPPWSPRPLEATAPT 180
DB 121 RFVQNTISRLLQETSEQVLAALKPWITRONFSRCLELOCOPDSSSTLPPWSPRPLEATAPT 180
QY 181 APQPPILLLLLPVGLLLAAACLMHQRTRRRPRRGEQVPPVPSQDILLVEH 235
DB 181 APQPPILLLLLPVGLLLAAACLMHQRTRRRPRRGEQVPPVPSQDILLVEH 235

RESULT 2
US-09-448-378-1
Sequence 1, Application US/09448378
Patent No. US20020034517A1
GENERAL INFORMATION:
APPLICANT: Brasel, Kenneth
TITLE OF INVENTION: Dendritic Cell Stimulatory Factor
FILE REFERENCE: 2836-D
CURRENT APPLICATION NUMBER: US/09/448,378
CURRENT FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-448-378-1

Query Match 100.0%; Score 1242; DB 10; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFOHSPISDPFAVKIRELSYLLQDYVTV 60
DB 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFOHSPISDPFAVKIRELSYLLQDYVTV 60
QY 61 ASNLQDEELCGGLMRVLVLAORRMERLKTVAAGSKMOGLLEEVNTEIHFTKCAEQPPPSCL 120
DB 61 ASNLQDEELCGGLMRVLVLAORRMERLKTVAAGSKMOGLLEEVNTEIHFTKCAEQPPPSCL 120
QY 121 RFVQNTISRLLQETSEQVLAALKPWITRONFSRCLELOCOPDSSSTLPPWSPRPLEATAPT 180
DB 121 RFVQNTISRLLQETSEQVLAALKPWITRONFSRCLELOCOPDSSSTLPPWSPRPLEATAPT 180
QY 181 APQPPILLLLLPVGLLLAAACLMHQRTRRRPRRGEQVPPVPSQDILLVEH 235
DB 181 APQPPILLLLLPVGLLLAAACLMHQRTRRRPRRGEQVPPVPSQDILLVEH 235

RESULT 3
US-09-983-806-6

Sequence 6, Application US/09983806
Patent No. US20020107365A1
GENERAL INFORMATION:
APPLICANT: Beckmann, M. Patricia

TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/983,806
FILING DATE: 25-Oct-2001
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/444,626
FILING DATE: 19-MAY-1995
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-983-806-6

Query Match 100.0%; Score 1242; DB 10; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFOHSPISDPFAVKIRELSYLLQDYVTV 60
DB 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFOHSPISDPFAVKIRELSYLLQDYVTV 60
QY 61 ASNLQDEELCGGLMRVLVLAORRMERLKTVAAGSKMOGLLEEVNTEIHFTKCAEQPPPSCL 120
DB 61 ASNLQDEELCGGLMRVLVLAORRMERLKTVAAGSKMOGLLEEVNTEIHFTKCAEQPPPSCL 120
QY 121 RFVQNTISRLLQETSEQVLAALKPWITRONFSRCLELOCOPDSSSTLPPWSPRPLEATAPT 180
DB 121 RFVQNTISRLLQETSEQVLAALKPWITRONFSRCLELOCOPDSSSTLPPWSPRPLEATAPT 180
QY 181 APQPPILLLLLPVGLLLAAACLMHQRTRRRPRRGEQVPPVPSQDILLVEH 235
DB 181 APQPPILLLLLPVGLLLAAACLMHQRTRRRPRRGEQVPPVPSQDILLVEH 235

RESULT 4

US-09-904-536-1
: Sequence 1, Application US/09904536
: Patent No. US20020111475A1
: GENERAL INFORMATION:
: APPLICANT: McGrath, Thomas J.
: APPLICANT: McGrew, Jeffrey T.
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03260.0028
: CURRENT APPLICATION NUMBER: US/09/904,536
: CURRENT FILING DATE: 2001-07-16
: PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
: PRIOR FILING DATE: 1999-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Patentln Ver. 2.1
: SEQ ID NO 1
: LENGTH: 235
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-904-536-1
Query Match 100.0%; Score 1242; DB 10; Length 235;
Best Local Similarity 100.0%; Pred. No. 1,4e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVALPANSPTTYLLLLSSGSLGTDGCSFQHSPISSDFAVKIRELSYLLQDYPTV
DB 1 MTVALPANSPTTYLLLLSSGSLGTDGCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
QY 61 ASNLQDELCGGLMRLVLAQRMERLKTIVAGSKMGGLLERVTETHFYTKCAFQPPSCL 120
DB 61 ASNLQDELCGGLMRLVLAQRMERLKTIVAGSKMGGLLERVTETHFYTKCAFQPPSCL 120
QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQCPDSSSTLPMPSPRLATAPT 180
DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQCPDSSSTLPMPSPRLATAPT 180
QY 181 APQPLLILLPVGLLLAAACMLHMORTRRTRPRGEOVPVPSPODLLVEH 235
DB 181 APQPLLILLPVGLLLAAACMLHMORTRRTRPRGEOVPVPSPODLLVEH 235
RESULT 5
US-09-904-536-10
: Sequence 10, Application US/09904536
: Patent No. US20020111475A1
: GENERAL INFORMATION:
: APPLICANT: McGrath, Thomas J.
: APPLICANT: McGrew, Jeffrey T.
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03260.0028
: CURRENT APPLICATION NUMBER: US/09/904,536
: CURRENT FILING DATE: 2001-07-16
: PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
: PRIOR FILING DATE: 1999-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Patentln Ver. 2.1
: SEQ ID NO 10
: LENGTH: 212
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-904-536-10
Query Match 90.5%; Score 1124; DB 10; Length 212;
Best Local Similarity 100.0%; Pred. No. 3e-91;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 SGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTVVASNLQDELCGGLMRLVLAQRMWE 84
DB 2 SGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTVVASNLQDELCGGLMRLVLAQRMWE 84
QY 85 RLKTVAGSKMGGLLERVTETHFYTKCAFQPPSCLRFVQTNISRLQETSEQLVALKPW 144
DB 62 RLKTVAGSKMGGLLERVTETHFYTKCAFQPPSCLRFVQTNISRLQETSEQLVALKPW 121

QY 145 ITRONFSRCLQCPDSSSTLPMPSPRLATAPTAPQPLLILLPVGLLLAAAC 204
DB 122 ITRONFSRCLQCPDSSSTLPMPSPRLATAPTAPQPLLILLPVGLLLAAAC 181
QY 205 LHMORTRRTRPRGEOVPVPSPODLLVEH 235
DB 182 LHMORTRRTRPRGEOVPVPSPODLLVEH 212
RESULT 6
US-09-904-536-18
: Sequence 18, Application US/09904536
: Patent No. US20020111475A1
: GENERAL INFORMATION:
: APPLICANT: McGrath, Thomas J.
: APPLICANT: McGrew, Jeffrey T.
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03260.0028
: CURRENT APPLICATION NUMBER: US/09/904,536
: CURRENT FILING DATE: 2001-07-16
: PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
: PRIOR FILING DATE: 1999-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Patentln Ver. 2.1
: SEQ ID NO 18
: LENGTH: 209
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-904-536-18
Query Match 89.7%; Score 1114; DB 10; Length 209;
Best Local Similarity 100.0%; Pred. No. 2.2e-90;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVVASNLQDELCGGLMRLVLAQRMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVVASNLQDELCGGLMRLVLAQRMERL 60
QY 87 KTVAGSKMGGLLERVTETHFYTKCAFQPPSCLRFVQTNISRLQETSEQLVALKPWIT 146
DB 61 KTVAGSKMGGLLERVTETHFYTKCAFQPPSCLRFVQTNISRLQETSEQLVALKPWIT 120
QY 147 RONFSRCLQCPDSSSTLPMPSPRLATAPTAPQPLLILLPVGLLLAAACMLH 206
DB 121 RONFSRCLQCPDSSSTLPMPSPRLATAPTAPQPLLILLPVGLLLAAACMLH 180
QY 207 WORTRRTRPRGEOVPVPSPODLLVEH 235
DB 181 WORTRRTRPRGEOVPVPSPODLLVEH 209
RESULT 7
US-09-904-536-9
: Sequence 9, Application US/09904536
: Patent No. US20020111475A1
: GENERAL INFORMATION:
: APPLICANT: McGrath, Thomas J.
: APPLICANT: McGrew, Jeffrey T.
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03260.0028
: CURRENT APPLICATION NUMBER: US/09/904,536
: CURRENT FILING DATE: 2001-07-16
: PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
: PRIOR FILING DATE: 1999-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Patentln Ver. 2.1
: SEQ ID NO 9
: LENGTH: 209
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-904-536-9

Query Match 89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 5e-90;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

27 TODCSFQHSPISSDFPAVKIRELSYLLQDYPVYVNASNLQDEELCGGLRWLVLAORMERL 86
1 TODCSFQHSPISSDFPAVKIRELSYLLQDYPVYVNASNLQDEELCGGLRWLVLAORMERL 60

87 KTVAGSKMÖGILLERVNTEIHFTVCARFQPPSCILRFVOTNISRLLOETSEQVVALKPWIT 146
61 KTVAGSKMÖGILLERVNTEIHFTVCARFQPPSCILRFVOTNISRLLOETSEQVVALKPWIT 120

147 RONSRCLELOCOPDSSITLPPMSPRPLEATAPAPOPPLLLLLLPVGLLLAAACGLH 206
121 RONSRCLELOCOPDSSITLPPMSPRPLEATAPAPOPPLLLLLLPVGLLLAAACGLH 180

207 WQTRRRTPRPGEQVPVPSQDILLVEH 235
181 WQTRRRTPRPGEQVPVPSQDILLVEH 209

RESULT 8
US-09-904-536-12
Sequence 12, Application US/09904536
Patent No. US20020111475A1
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 12
LENGTH: 209
TYPE: PR
ORGANISM: Homo sapiens
US-09-904-536-12

Query Match 89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 5e-90;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

27 TODCSFQHSPISSDFPAVKIRELSYLLQDYPVYVNASNLQDEELCGGLRWLVLAORMERL 86
1 TODCSFQHSPISSDFPAVKIRELSYLLQDYPVYVNASNLQDEELCGGLRWLVLAORMERL 60

87 KTVAGSKMÖGILLERVNTEIHFTVCARFQPPSCILRFVOTNISRLLOETSEQVVALKPWIT 146
61 KTVAGSKMÖGILLERVNTEIHFTVCARFQPPSCILRFVOTNISRLLOETSEQVVALKPWIT 120

147 RONSRCLELOCOPDSSITLPPMSPRPLEATAPAPOPPLLLLLLPVGLLLAAACGLH 206
121 RONSRCLELOCOPDSSITLPPMSPRPLEATAPAPOPPLLLLLLPVGLLLAAACGLH 180

207 WQTRRRTPRPGEQVPVPSQDILLVEH 235
181 WQTRRRTPRPGEQVPVPSQDILLVEH 209

RESULT 9
US-09-904-536-14
Sequence 14, Application US/09904536
Patent No. US20020111475A1
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536

CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 14
LENGTH: 209
TYPE: PR
ORGANISM: Homo sapiens
US-09-904-536-14

Query Match 89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 5e-90;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

27 TODCSFQHSPISSDFPAVKIRELSYLLQDYPVYVNASNLQDEELCGGLRWLVLAORMERL 86
1 TODCSFQHSPISSDFPAVKIRELSYLLQDYPVYVNASNLQDEELCGGLRWLVLAORMERL 60

87 KTVAGSKMÖGILLERVNTEIHFTVCARFQPPSCILRFVOTNISRLLOETSEQVVALKPWIT 146
61 KTVAGSKMÖGILLERVNTEIHFTVCARFQPPSCILRFVOTNISRLLOETSEQVVALKPWIT 120

147 RONSRCLELOCOPDSSITLPPMSPRPLEATAPAPOPPLLLLLLPVGLLLAAACGLH 206
121 RONSRCLELOCOPDSSITLPPMSPRPLEATAPAPOPPLLLLLLPVGLLLAAACGLH 180

207 WQTRRRTPRPGEQVPVPSQDILLVEH 235
181 WQTRRRTPRPGEQVPVPSQDILLVEH 209

RESULT 10
US-09-904-536-17
Sequence 17, Application US/09904536
Patent No. US20020111475A1
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 17
LENGTH: 209
TYPE: PR
ORGANISM: Homo sapiens
US-09-904-536-17

Query Match 89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 5e-90;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

27 TODCSFQHSPISSDFPAVKIRELSYLLQDYPVYVNASNLQDEELCGGLRWLVLAORMERL 86
1 TODCSFQHSPISSDFPAVKIRELSYLLQDYPVYVNASNLQDEELCGGLRWLVLAORMERL 60

87 KTVAGSKMÖGILLERVNTEIHFTVCARFQPPSCILRFVOTNISRLLOETSEQVVALKPWIT 146
61 KTVAGSKMÖGILLERVNTEIHFTVCARFQPPSCILRFVOTNISRLLOETSEQVVALKPWIT 120

147 RONSRCLELOCOPDSSITLPPMSPRPLEATAPAPOPPLLLLLLPVGLLLAAACGLH 206
121 RONSRCLELOCOPDSSITLPPMSPRPLEATAPAPOPPLLLLLLPVGLLLAAACGLH 180

207 WQTRRRTPRPGEQVPVPSQDILLVEH 235
181 WQTRRRTPRPGEQVPVPSQDILLVEH 209

RESULT 11
US-09-904-536-11
Sequence 11, Application US/09904536
Patent No. US2002011475A1
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-904-536-11

Query Match 89.2%; Score 1108; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 7.4e-90;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 1 TODCSFOHSPISDFAVKIRELSDYLLQDYPYTVASNLQDEELCGGLMRVLAQRMERL 86
QY 87 KTVAGSKMOGLLEERVNTEIHFTVTCAPQPPSCLEFVQTNISRLQETSEQLVALKPWIT 146
Db 61 KTVAGSKMOGLLEERVNTEIHFTVTCAPQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120
QY 147 RQNSRCLELQCPDSSSTLPWPMSRPLEATAPTAPOPLLILLPVGLLLAAACMH 206
Db 121 RQNSRCLELQCPDSSSTLPWPMSRPLEATAPTAPOPLLILLPVGLLLAAACMH 180
QY 207 WQTRRRTPRGEQVPPVPSPODLLVEH 235
Db 181 WQTRRRTPRGEQVPPVPSPODLLVEH 209

RESULT 12
US-09-904-536-15
Sequence 15, Application US/09904536
Patent No. US2002011475A1
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-904-536-15

Query Match 89.2%; Score 1108; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 7.4e-90;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 27 TODCSFOHSPISDFAVKIRELSDYLLQDYPYTVASNLQDEELCGGLMRVLAQRMERL 86
Db 1 TODCSFOHSPISDFAVKIRELSDYLLQDYPYTVASNLQDEELCGGLMRVLAQRMERL 60
QY 87 KTVAGSKMOGLLEERVNTEIHFTVTCAPQPPSCLEFVQTNISRLQETSEQLVALKPWIT 146

Db 61 KTVAGSKMOGLLEERVNTEIHFTVTCAPQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120
QY 147 RQNSRCLELQCPDSSSTLPWPMSRPLEATAPTAPOPLLILLPVGLLLAAACMH 206
Db 121 RQNSRCLELQCPDSSSTLPWPMSRPLEATAPTAPOPLLILLPVGLLLAAACMH 180
QY 207 WQTRRRTPRGEQVPPVPSPODLLVEH 235
Db 181 WQTRRRTPRGEQVPPVPSPODLLVEH 209

RESULT 13
US-09-904-536-13
Sequence 13, Application US/09904536
Patent No. US2002011475A1
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-904-536-13

Query Match 89.1%; Score 1107; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 9.1e-90;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFOHSPISDFAVKIRELSDYLLQDYPYTVASNLQDEELCGGLMRVLAQRMERL 86
Db 1 TODCSFOHSPISDFAVKIRELSDYLLQDYPYTVASNLQDEELCGGLMRVLAQRMERL 60
QY 87 KTVAGSKMOGLLEERVNTEIHFTVTCAPQPPSCLEFVQTNISRLQETSEQLVALKPWIT 146
Db 61 KTVAGSKMOGLLEERVNTEIHFTVTCAPQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120
QY 147 RQNSRCLELQCPDSSSTLPWPMSRPLEATAPTAPOPLLILLPVGLLLAAACMH 206
Db 121 RQNSRCLELQCPDSSSTLPWPMSRPLEATAPTAPOPLLILLPVGLLLAAACMH 180
QY 207 WQTRRRTPRGEQVPPVPSPODLLVEH 235
Db 181 WQTRRRTPRGEQVPPVPSPODLLVEH 209

RESULT 14
US-09-904-536-8
Sequence 8, Application US/09904536
Patent No. US2002011475A1
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens

US-09-904-536-8

| | | | | |
|---------------------------|--------|--------------------|-----------|-------------|
| Query Match | 89.08; | Score 1106; | DB 10; | Length 209; |
| Best Local Similarity | 99.58; | Pred. No. 1.1e-89; | | |
| Matches 208; Conservative | 0; | Mismatches 1; | Indels 0; | Gaps 0; |

27 TQDCSFQHSPTSSDFAVKIRELSDYLQDYPVATASNLQDEELCGGLMRLVLAQRMMERL 86
 1 TQDCSFQHSPTSSDFAVKIRELSDYLQDYPVATASNLQDEELCGGLMRLVLAQRMMERL 60

Qy 87 KTVAGSKMGLLERVNTVEIHFTVKCAQPPSPCLRFVQVNIISRLQETSQDVALKPWIT 146
 |||||
 Dd 61 KTVAGSKMGLLERVNTVEIHFTVKCAQPPSPCLRFVQVNIISRLQETSQDVALKPWIT 120

QY 147 RQNSRCLLEQCQPBSSTLPWPSPRLPEATAPAQPELLLLLLPVGLLAAACGH.206
|||
Db 121 RQNSRCLLEQCQPDSSTLPWPSPRLPEATAPAQPELLLLLLPVGLLAAACGH.180

| | | | | |
|--|----|-----|-----------------------------|-----|
| | QY | 207 | WQTRRRRTPRGEGVPPVPSPDQLLVEH | 235 |
| | | | | |
| | | | | |
| | Dd | 181 | WQTRRRRTPRGEGVPPVPSPDQLLVEH | 209 |

RESULT 15

US-09-904-536-16

Sequence 16, Application US/09904536

Patent No. US2002011475A1

; GENERAL INFORMATION:

APPLICANT: Graddis, Thomas J.

APPLICANT: McGrew, Jeffrey T

1. TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE

FILE REFERENCE: 03260.0028

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; CURRENT FILING DATE: 2001-07-16

PRIOR APPLICATION: 09/109,100

PRIOR FILING DATE: 1999-07-02

NUMBER OF SEQ ID NOS: 20

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; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 16

LENGTH: 209

TYPE: PRT

ORGANISM: *Homo sapiens*

ORGANISM: HU
US-09-904-536-16

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|---------------------------|--------|--------------------|-----------|-------------|
| Query Match | 88.6%; | Score 1100; | DB 10; | Length 209; |
| Best Local Similarity | 99.5%; | Pred. No. 3.8e-89; | | |
| Matches 208; Conservative | 0; | Mismatches 1; | Indels 0; | Gaps 0; |

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0Y 27 TDQDSFQHSPISSDFAVKIRELSDYLLQDYPVTASNLODEELCGGLRLVLAQRMERL 86
|||||
Db 1 TDQDSFQHSPISSDFAVKIRELSDYLLQDYPVTASNLODEELCGGLRLVLAQRMERL 60

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QY 87 KTVAGSKMGLLERVNTIEIHFVTKCAFPSPSCURFVOTNISRLLOETSEDLVALKPMIT 146
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 KTVAGSKMGLLERVNTIEIHFVTKCAFPSPSCURFVQNISRLLOETSEDLVALKPRIT 120

Dy 147 RQNSRCLFQCQPSSSTLPWPSPRLVETAPAPQLLLLLLVGLLLAAWCLH 206
 |||||
Dd 121 RQNSRCLFQCQPSSSTLPWPSPRLVETAPAPQLLLLLLVGLLLAAWCLH 180

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QY 207 WQTRRRRTPRPGEQVPVPVSPQDLLVEH 235
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Db 181 WQTRRRRTPRPGEQVPVPVSPQDLLVEH 209
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Search completed: May 27, 2003, 18:36:27
Job time : 58 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 27, 2003, 18:25:26 ; Search time 11 Seconds

(without alignments)
886.085 Million cell updates/sec

Title: US-08-994-468-6

Sequence: 1 MTVLAPAMSPPTTYLLLLLL.....RPGQVPPVPQDQLLVH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match Length | ID | Description |
|------------|-------|-------|--------------|---------------|---------------------|
| 1 | 1242 | 100.0 | 235 | 1 FLJL_HUMAN | P49771 homo sapien |
| 2 | 768 | 61.8 | 232 | 1 FLJL_MOUSE | P49772 mus musculus |
| 3 | 92 | 7.4 | 661 | 1 AT12_VZVD | P09264 varicella-z |
| 4 | 89.5 | 7.2 | 941 | 1 GBR2_HUMAN | O75899 homo sapien |
| 5 | 89 | 7.2 | 387 | 1 SGCA_MESAU | O64255 mesocricetu |
| 6 | 89 | 7.2 | 793 | 1 S3AI_HUMAN | O15453 homo sapien |
| 7 | 87.5 | 7.0 | 415 | 1 TNR3_MOUSE | P50284 mus musculus |
| 8 | 87.5 | 7.0 | 479 | 1 MIP1_DROME | P20453 drosophila |
| 9 | 87 | 7.0 | 910 | 1 DDRI_RAT | O63474 rattus norv |
| 10 | 87 | 7.0 | 911 | 1 DDRI_MOUSE | O03146 mus musculus |
| 11 | 86.5 | 7.0 | 1394 | 1 CNG4_BOVIN | O28181 bos taurus |
| 12 | 86 | 6.9 | 485 | 1 SSGP_VOLCA | P21997 volvox cart |
| 13 | 85 | 6.8 | 282 | 1 ATFS_HUMAN | O91261 homo sapien |
| 14 | 85 | 6.8 | 366 | 1 FCGN_RAT | P13599 rattus norv |
| 15 | 84.5 | 6.8 | 3726 | 1 ABFL_MOUSE | O61329 mus musculus |
| 16 | 84 | 6.8 | 582 | 1 MNT_HUMAN | O99583 homo sapien |
| 17 | 84 | 6.8 | 732 | 1 YF48_HUMAN | O9H044 homo sapien |
| 18 | 84 | 6.8 | 1234 | 1 YF48_MOUSE | O9H044 rattus norv |
| 19 | 83.5 | 6.7 | 671 | 1 Z282_HUMAN | O9H047 homo sapien |
| 20 | 83 | 6.7 | 758 | 1 VKG2_HUMAN | P38435 homo sapien |
| 21 | 82 | 6.6 | 2167 | 1 SHK1_RAT | O6WV48 rattus norv |
| 22 | 81.5 | 6.6 | 488 | 1 MNT_HUMAN | P24347 homo sapien |
| 23 | 81.5 | 6.6 | 591 | 1 MNT_MOUSE | O08789 mus musculus |
| 24 | 81.5 | 6.6 | 2124 | 1 Y192_HUMAN | O93074 homo sapien |
| 25 | 81 | 6.5 | 283 | 1 ATFS_MOUSE | O70101 mus musculus |
| 26 | 81 | 6.5 | 387 | 1 SGCA_MOUSE | P82350 mus musculus |
| 27 | 81 | 6.5 | 428 | 1 EPC_HUMAN | P01854 homo sapien |
| 28 | 81 | 6.5 | 1248 | 1 DIAL_HUMAN | O60610 homo sapien |
| 29 | 80.5 | 6.5 | 1402 | 1 IF4G_RABIT | P11110 oryctolagus |
| 30 | 80 | 6.4 | 397 | 1 CEPD_STRCL | P18549 streptomyces |
| 31 | 80 | 6.4 | 940 | 1 GBR2_RAT | O68871 rattus norv |
| 32 | 80 | 6.4 | 1174 | 1 KPC1_COCHOE | O42632 cochliodon |
| 33 | 80 | 6.4 | 1794 | 1 YAVI_SCHPO | O10172 schistosach |

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| 34 | 79 | 6.4 | 805 | 1 YGM6_YEAST | P53086 saccharomyc |
| 35 | 78.5 | 6.3 | 251 | 1 HXB4_HUMAN | P17483 homo sapien |
| 36 | 78.5 | 6.3 | 382 | 1 AYRB_RAT | P38445 rattus norv |
| 37 | 78.5 | 6.3 | 387 | 1 SGCA_RABIT | O28686 oryctolagus |
| 38 | 78.5 | 6.3 | 913 | 1 DDRI_HUMAN | O08345 h epithelia |
| 39 | 78.5 | 6.3 | 1180 | 1 ATY1_HUMAN | O9H041 homo sapien |
| 40 | 78 | 6.3 | 205 | 1 CYSR_SYNY3 | O55854 synechocyst |
| 41 | 78 | 6.3 | 566 | 1 TS13_MOUSE | O01755 mus musculus |
| 42 | 77.5 | 6.2 | 341 | 1 PLSX_VIRCH | O9K044 vibrrio chol |
| 43 | 77.5 | 6.2 | 1885 | 1 FAS2_CANAL | P43098 c fatty aci |
| 44 | 77.5 | 6.2 | 2004 | 1 MOZ_HUMAN | O92794 homo sapien |
| 45 | 77 | 6.2 | 195 | 1 CORA_HPBVF | P29178 hepatitis b |

ALIGNMENTS

RESULT 1
FLJL_HUMAN
ID FLJL_HUMAN STANDARD: PRT: 235 AA.
AC P49771;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3
DE ligand) (Flt3L).
GN FLT3LG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP MEDLINE=94195428; PubMed=8145851;
RX MEDLINE=94235842; PubMed=8180375;
RA Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,
RA Bazan J.F., Kastelein R., Hudak S., Wagner J., Matson J., Luh J.,
RA Duda G., Martina N., Peterson D., Menon S., Shanale A.,
RA Muench M., Keilner G., Namikawa R., Renick D., Roncarolo M.G.,
RA Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.;
RT "Ligand for Flt3/Flk2 receptor tyrosine kinase regulates growth of
RT haematopoietic stem cells and is encoded by variant RNAs.";
RL Nature 368:643-648(1994).
[2]
RP MEDLINE=94235842; PubMed=8180375;
RX Hannum S.D., James L., Johnson L., Brasel K., de Vries P.,
RA Escobar S.S., Downey H., Splet R.R., Beckmann M.P., McKenna H.J.;
RT "Cloning of the human homologue of the murine Flt3 ligand: a growth
RT factor for early hematopoietic progenitor cells.";
RL Blood 83:2795-2801(1994).
[3]
RP MEDLINE=96032581; PubMed=7566977;
RX Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
RA Escobar S.;
RT "Structural analysis of human and murine Flt3 ligand genomic loci.";
RL Oncogene 11:1165-1172(1995).
[4]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=20343011; PubMed=10881197;
RA Savvides S.N., Boone T., Karplus P.A.;
RT "Flt3 ligand structure and unexpected commonalities of helical
RT bundles and cystine knots.";
RL Nat. Struct. Biol. 7:486-491(2000).
-I- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
CC FACTORS AND INTERLEUKINS.
CC -I- SUBUNIT: Homodimer (isoform 2).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
CC secreted (isoform 2).
CC -I- ALTERNATIVE PRODUCTS: 2 isoforms: a 1/membrane-bound (shown here)
CC and 2/soluble; are produced by alternative splicing.

FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 232 SL CYTOKINE.
 FT DOMAIN 27 189 EXTRACELLULAR (POTENTIAL).
 FT TRASMEM 190 210 POTENTIAL.
 FT DOMAIN 211 232 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 31 112 BY SIMILARITY.
 FT DISULFID 71 156 BY SIMILARITY.
 FT DISULFID 120 161 BY SIMILARITY.
 FT CARBOHYD 127 127 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 152 152 DDTLLPPSPALTEATELPEPRROLLELLELTLV
 FT VARSPLIC 164 232 LAAAGLRWQARARRGELHPGVLPSPH -> GNGPRAOH
 FT VARSPLIC 164 232 HGATRLTATLTCVCGLLPLVGTSHMEFFELFSLSSF
 FT VARSPLIC 164 232 LKMYLV (IN ISOFORM 2).
 FT VARSPLIC 164 232 DDTLL (IN ISOFORM 3).
 FT VARSPLIC 164 232 MISSING (IN ISOFORM 4).
 FT VARSPLIC 164 232 VOCOP -> GLIMQARTLNKSSCLSVLSACIT (IN
 FT VARSPLIC 164 232 ISOFORM 4).
 FT CONFLICT 141 141 A -> G (IN REF. 1).
 FT CONFLICT 198 198 MISSING (IN REF. 2).
 SQ SEQUENCE 232 AA: 26141 MW: 3A3680D3CB69FBA6 CRC64:

Query Match 61.8%; Score 768; DB 1; Length 232;
 Best Local Similarity 70.0%; Pred. No. 3.6e-57;
 Matches 163; Conservative 17; Mismatches 43; Indels 10; Gaps 4;

OY 1 MYVLAPWSP-TTYLLLLLSGLSGTODCSFQSPISDFAVKIRELSDYLLQDYPVT 59
 DB 1 MYVLAPWSPNSLLLLLSPLCLGTPDCYRSHSPISSEFKVKKRELTDHLKDYPT 60
 OY 60 VASNLQDEELGGLMRVLAQRMERLKTAVGSKMOGLLEERVTEIHFVTKCAFPSPSC 119
 DB 61 VAVNLQDEKCKKALMSLFLAQRWIEQDKTVAGSKMOTLEDVNTETHEFVTSCEFOPLC 120
 OY 120 LRVQVNIISRLQETSEQLVALKPMYTR--QNSRCLQLOCCQDSSLPSPSPRPLEAT 177
 DB 121 LRVQVNIISRLQETSEQLVALKPMYTR--QNSRCLQLOCCQDSSLPSPSPRPLEAT 180
 OY 178 APTAPQP---LLELLLPVGLLLLAAMCLHMORTRRTPRPGEQVPVPSPP 227
 DB 181 ELPEPRRQLLLLLLLPLTLVLLAAMCLRMQRARR---GELHPGVPLP 223

RESULT 3
 AT12_VZVD STANDARD: PRT: 661 AA.
 AC P09264:

DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last annotation update)
 DE Alpha trans-inducing factor 74 kDa protein.
 GN 12.
 OS Varicella-zoster virus (strain Dumas) (VZV).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.
 OX NCBI_Taxid=10338;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86306657; PubMed=3018124;
 RA Davison A.J., Scott J.E.;
 RT "The complete DNA sequence of varicella-zoster virus.";
 RL J. Gen. Virol. 67:1759-1816(1986).
 -1- FUNCTION: MODULATE ALPHA TRANS-INDUCING FACTOR-DEPENDENT
 ACTIVATION OF ALPHA GENES.

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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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DR EMBL: X04370; CAA27895.1; -.
 DR PIR: C27342; TNBE12.
 DR InterPro: IPR005051; Herpes_UL46.
 DR Pfam: PF03387; Herpes_UL46; 1.
 KW Transcription regulation; Trans-acting factor.
 SQ SEQUENCE 661 AA: 74272 MW: C5CA77A16D365379 CRC64:

Query Match 7.4%; Score 92; DB 1; Length 661;
 Best Local Similarity 26.6%; Pred. No. 2.7; Indels 36; Gaps 11;
 Matches 61; Conservative 29; Mismatches 36;

OY 19 LLSSGLSGTODCS---FQHSPISSDFAVKIRELSDYLLQDYPVTASNLQDEELCG- 71
 DB 79 LTPSVLQSTERRHSLVGLGHHNNVPESLVVSGMSNDVHGFQRMVETIQCLDLKLSGD 138
 OY 72 GLMRVLAQRMERLKTAVGSKMOGLLEERVTEIHFVTKCAFP---PSCIRFV 123
 DB 139 GLW-WVYENTYWOYLKTYTAEVPTSEKVKSKSTVLLFSSVVAKPISRHPFKSKYI 197
 OY 124 QTNISRLQETSEQLVALKPMYTRQNSRCLQLOCCQDSSLPSPSPRPLEATAPAP 182
 DB 198 NSDYRGICQELREALGAVQKYM---YFMR-----PDDPTNPSPTIRINQETIAATAT 247
 OY 183 QPPLLLLLLPVGLLLLAAMCLHMORTRRTPRPGEQVPVPSPPDLL 231
 DB 248 GYGMWLFLLVDV---ARVCRLKLQFRIRICPRASV---IPDLL 287

RESULT 4
 GBR2_HUMAN

ID GBR2_HUMAN STANDARD: PRT: 941 AA.
 AC G75899; O75974; O75975; Q9UN99; Q9UNR1; Q9PIR2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Receptor-aminobutyric acid type B receptor, subunit 2 precursor (GABA-B
 DE 51) (GPR 51) (HG20).
 GN GABBR2 OR GPR51.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN 11
 RP SEQUENCE FROM N.A. (ISOFORM 2A).
 RC TISSUE=Cerebellum;
 RX MEDLINE=99087321; PubMed=9872316;
 RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,
 RA Barnes A.A., Emson P., Ford S.M., Marshall F.H.;
 RT "Heterodimerization is required for the formation of a functional
 RT GABA(B) receptor.";
 RL Nature 396:679-682(1998).
 RN 121
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2A; 2B AND 2C).
 RC TISSUE=Brain;
 RX MEDLINE=20193514; PubMed=10727622;
 RA Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
 RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";
 RL Brain Res. 860:41-52(2000).
 RN 131
 RP SEQUENCE FROM N.A. (ISOFORM 2A).
 RA Liu M., Parker R., McCrear K., Watson J., Baker E., Sutherland G.,
 RA Herzog H.;
 RT "Cloning and characterization of a novel human GABA-B receptor subtype
 RT with high affinity for GABA and low affinity for baclofen.";
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN 141
 RP SEQUENCE FROM N.A. (ISOFORM 2A).
 RC TISSUE=Hippocampus;
 RA Borowsky B., Laz T., Gerald C.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN 151
 RP SEQUENCE FROM N.A. (ISOFORM 2A).

CC TISSUE=Fetal brain; PubMed=10087195;
RX MEDLINE=99189236;
RA NG G.Y.K., McDonald T., Bonnett T., Rigby M., Heavens R., Whiting P.,
RA Chateauneuf A., Coulombe N., Kargman S., Caskey T., Evans J.F.,
RA O'Neill G.P., Liu Q.;
RT "Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAB
RT receptors expressed predominantly in nervous tissues and mapped
RT proximal to the hereditary sensory neuropathy type 1 locus on
RT chromosome 9";
RL Genomics 56:288-295(1999).
RN [6].
RP SEQUENCE FROM N.A. (ISOFORM 2A), AND VARIANTS PHE-628 AND ALA-869.
RC TISSUE=Brain;
RX MEDLINE=99263199; PubMed=10328880;
RA Martin S.C., Russek S.J., Farb D.H.;
RT "Molecular identification of the human GABABR2: cell surface
RT expression and coupling to adenylyl cyclase in the absence of
RT GABABR1";
RL Mol. Cell. Neurosci. 13:180-191(1999).
RN [7].
RP R1A-R2 INTERACTION.
RX MEDLINE=99175124; PubMed=10075644;
RA NG G.Y.K., Clark J., Coulombe N., Ether N., Hebert T.E., Sullivan R.,
RA Kargman S., Chateauneuf A., Tsukamoto N., McDonald T., Whiting P.,
RA Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
RA Bonner T.I., O'Neill G.P.;
RT "Identification of a GABAB receptor subunit, gpb2, required for
RT functional GABAB receptor activity";
RL J. Biol. Chem. 274:7607-7610(1999).
RN [8].
RP R1A-R2 INTERACTION.
RX MEDLINE=20237752; PubMed=10773016;
RA Sullivan R., Chateauneuf A., Coulombe N., Kolakowski L.F. Jr.,
RA Johnson M.P., Hebert T.E., Ether N., Belley M., Metters K.,
RA Abramovitz M., O'Neill G.P., NG G.Y.K.;
RT "Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B))
RT receptors with truncated receptors and metabotropic glutamate
RT receptor 4 supports the GABA(B) heterodimer as the functional
RT receptor";
RL J. Pharmacol. Exp. Ther. 293:460-467(2000).
RN [9].
RP FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
RX MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM CHANNELS AND MODULATES
CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
CC FINE-TUNING OF INHIBITOR SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
CC ANTIHYPNOSIS.
RN [10].
RP SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
RX IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
CC HAPPEN.
CC [11].
RP SUBCELLULAR LOCATION: INTERAL MEMBRANE PROTEIN. MOREOVER
RX COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
CC PLASMA MEMBRANE.
RN [12].
RP ALTERNATIVE PRODUCTS. 3 ISOFORMS: 2A (SHOWN HERE), 2B AND 2C; ARE
RX PRODUCED BY ALTERNATIVE SPLICING.
CC [13].
RP TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN
RX CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND
CC TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS
CC CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALE AND MEDULLA.
CC WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.
RN [14].
RP DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
RX MEDIATE HETERO DIMERIC INTERACTION WITH GABA-B RECEPTOR 1.
CC [15].
RP SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
RX GABA-B RECEPTOR SUBFAMILY.
CC [16].
RP [17].
RX [18].
CC [19].
CC [20].
CC [21].
CC [22].
CC [23].
CC [24].
CC [25].
CC [26].
CC [27].
CC [28].
CC [29].
CC [30].
CC [31].
CC [32].
CC [33].
CC [34].
CC [35].
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CC [80].
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CC [82].
CC [83].
CC [84].
CC [85].
CC [86].
CC [87].
CC [88].
CC [89].
CC [90].
CC [91].
CC [92].
CC [93].
CC [94].
CC [95].
CC [96].
CC [97].
CC [98].
CC [99].
CC [100].

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[illegible]

RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Mux P.,
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton D., Goele D., Graves T., Hawkins J.,
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozerky P., Roloff J.,
 RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
 RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
 RA Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,
 RA McDevitt H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
 RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,
 RA Serousi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
 RA Wilkerson P., Bodetleitch A., Hartman K., Hu X., Khan A.S., Lane L.,
 RA Tilahun Y., Wright H.;
 RA "The DNA sequence of human chromosome 22.";
 RL Nature 402:489-495(1999).
 RN [3]
 RP CHARACTERIZATION OF THE SPLICEOSOME.
 RX MEDLINE:20337962; PubMed:10882114;
 RA Das R., Zhou Z., Reed R.;
 RT "Functional association of U2 snRNP with the ATP-independent
 RT spliceosomal complex E.";
 RL Mol. Cell 5:779-787(2000).
 CC -1- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A'
 CC COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE
 CC BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT
 CC BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS
 CC ESSENTIAL, IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE
 CC INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.
 CC -1- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3A WHICH IS COMPOSED OF
 CC THREE SUBUNITS: SF3A3/SAP61, SF3A2/SAP62, SF3A1/SAP14. SF3A
 CC ASSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TO
 CC FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP).
 CC INTERACTS WITH SF3A3.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.
 CC -1- SIMILARITY: CONTAINS 1 UBQUITIN-LIKE DOMAIN.
 CC -1- SIMILARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRP21.
 CC -----
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 CC -----
 DR EMBL: X85237; CA939494.1; -;
 DR EMBL: AC004997; AAC23435.1; -;
 DR HSSP: Q15843; INDD.
 DR GeneW: HGNC:10765; SF3A1.
 DR MIM: 605595; -;
 DR InterPro: IPR000061; Surp.
 DR InterPro: IPR000626; Ubiquitin.
 DR Pfam: PF00240; ubiquitin.1.
 DR SMART: SM00213; UBO; 1.
 DR PROSITE: PS50053; UBQUITIN_2; 1.
 KM Spliceosome: mRNA processing; mRNA splicing; Nuclear protein; Repeat.
 FT REPEAT 52 94 SURP MOTIF 1.
 FT REPEAT 166 208 SURP MOTIF 2.
 FT DOMAIN 707 793 UBQUITIN-LIKE.
 FT DOMAIN 10 16 POLY-PRO.
 FT DOMAIN 118 122 POLY-GLU.
 FT DOMAIN 260 267 POLY-GLU.
 FT DOMAIN 369 372 POLY-PRO.
 FT DOMAIN 557 560 POLY-PRO.
 FT DOMAIN 672 675 POLY-PRO.
 SQ SEQUENCE 793 AA; 88886 MW; 7259F1EC4577305C CRC64;
 Query Match 7.2%; Score 89; DB 1; Length 793;
 Best Local Similarity 22.3%; Pired. No. 5.8;
 Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

DB 401 LPPAPDELYL-----SPITGE---KI-----PASK 424
 QY 64 LODELGGMLRWLYAORWME-RLKTV-----AGSKOGLLERVNTEIHF 107
 DB 425 MOEIMRG-----LLDRWLEQRDRSIREKOSDDEYVAPGLDISSIKQLAER-RTIFG 478
 QY 108 VTKCA-----FQPPSCLEF-----VQTNISRLLOETSEGLVLRPMI 145
 DB 479 VEEFAIGKKIGEEELQKPEEKVTWDGSHGSMARQAAQANIT--LOEQLAIIHAKGLV 536
 QY 146 -----TRQNF--SRLELQCP-----DSSLTP-----PWSRPLEAT-----APT 180
 DB 537 PEDTKERIGPSKPEIEIPQPPSSATNIPSSAPITTSVPRPTMPPTVVSAPV 596
 QY 181 APQPLLLLLLPVGLLLLAAMCLHWQRT-----RTRPRGEQVP---VPS 227
 DB 597 MPRPMASVNLPPGSAVLAHPRIILHAPRINVMPSAPRIMAPRPPMIVPAFAVPAP 656
 RESULT 7
 TNR3 MOUSE STANDARD; PRT; 415 AA.
 ID TNR3 MOUSE
 AC P50284;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 3 precursor
 DE (lymphotoxin-beta receptor).
 GN LTRB OR TNFRSF3 OR TNFCR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN:CVB; TISSUE:Lung;
 RX MEDLINE:96072804; PubMed:7594541;
 RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 RA Browning J.L., Ware C.F.;
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 RT and expression.";
 RL J. Immunol. 155:5280-5286(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:96163885; PubMed:8586432;
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
 RA Honjo T.;
 RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
 RT sequence trap and chromosomal mapping.";
 RL Genomics 30:312-319(1995).
 CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 CC LTA and LTB, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
 CC and TRAF5. May play a role in the development of lymphoid organs
 CC (By similarity).
 CC -1- SUBUNIT: self-associates (By similarity).
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -----
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 CC -----
 DR EMBL: U29173; AAA68964.1; -;
 DR EMBL: L38423; AAB00846.1; -;
 DR EMBL: U30798; AAA81334.1; -;
 DR HSSP: O14763; IDOG.
 DR MCD: MGI:104875; Ltbr.
 DR InterPro: IPR001368; TNFR_c6.

DE (DDR) (Discoidin receptor tyrosine kinase) (Protein-tyrosine kinase
MPK-6).
DE DDRI OR EDDRI OR CAK OR MPK6.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
ON NCBI_TaxID=10090;
RX RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=C57BL/6;
RX MEDLINE=96204002; PubMed=8622863;
RA Perez J.L., Jing S.Q., Wong T.W.;
RT "Identification of two isoforms of the Cak receptor kinase that are
coexpressed in breast tumor cell lines.";
RL Oncogene 12:1469-1477(1996).
RN
RP SEQUENCE OF 766-822 FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Embryonic brain;
RX MEDLINE=93096484; PubMed=1281307;
RA Giliardi-Hebensstreit P., Nieto M.A., Frain M., Mattei M.-G.,
RA Chestier A., Wilkinson D.G., Charney P.;
RT "An Eph-related receptor protein tyrosine kinase gene segmentally
expressed in the developing mouse hindbrain.";
RL Oncogene 7:2499-2506(1992).
CC
CC -1- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND
RECOGNITION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CAK I (SHOWN HERE) AND CAK II;
ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER BY THE
ABSENCE OF A 37 RESIDUES SEGMENT.
CC -1- TISSUE SPECIFICITY: THE PREDOMINANT ISOFORM CAK I, IS EXPRESSED IN
DEVELOPING EMBRYO AND ADULT BRAIN; CAK II IS EXPRESSED IN VARIOUS
EPITHELIAL CELLS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
RECEPTOR SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
CC
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CC
EMBL: L57509; AAB05209.1; -;
EMBL: X57240; CA440516.1; -;
DR PIR: S30502; S30502.
DR HSSP: P00523; 2PTK.
DR MGD: MGI:99216; Ddr1.
DR InterPro: IPR000719; Euk.pkinase.
DR InterPro: IPR000421; FA58.C.
DR InterPro: IPR002011; RTKinaseIT.
DR InterPro: IPR001245; Tyr.pkinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00754; F5_F8_TypeC; 1.
DR Prodom: PD000001; Euk.pkinase; 1.
DR SMART: SM00231; FA58C; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_LI; 1.
DR PROSITE: PS01285; FA58C_1; 1.
DR PROSITE: PS01286; FA58C_2; 1.
KW Transferase; Tyrosine-protein kinase; Glycoprotein; Signal;
KW Phosphorylation; Transmembrane; Receptor; ATP-binding;
KW Alternative splicing.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 911 EPITHELIAL DISCOIDIN DOMAIN RECEPTOR 1.
FT DOMAIN 20 414 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 415 441 POTENTIAL.
FT DOMAIN 442 911 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 32 186 F5/8 TYPE C (PHOSPHOLIPID-BINDING,
POTENTIAL).
FT DOMAIN 379 413 GLY/PRO-RICH.
FT DOMAIN 474 599 GLY/PRO-RICH.
FT DOMAIN 608 902 PROTEIN KINASE.
FT NP_BIND 614 622 ATP (BY SIMILARITY).
FT BINDING 653 653 ATP (BY SIMILARITY).
FT ACT_SITE 764 764 ATP (BY SIMILARITY).
FT DISULFID 32 186 BY SIMILARITY.
FT MOD_RES 511 511 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 790 790 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 794 794 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 795 795 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 503 539 MISSING (IN ISOFORM CAK II).
SQ SEQUENCE 911 AA; 101160 MW; DB87FE03DD079510 CRC64;
Query Match 7.0%; Score 87; DB 1; Length 911;
Best Local Similarity 24.5%; Pred. No. 10;
Matches 38; Conservative 12; Mismatches 35; Indels 70; Gaps 9;
QY 143 PWITRONSRLQLQCGDSSSTLP-PPW---SPRLQNTA---PTAPQ----- 184
DB 357 PWLFESEISFISDV-VNDSSTFPAPWPPGPPPTNFSLELEPGQPVAKAGSPTA 415
QY 185 -----PULLLLLPVGLLLAAMCLHMOR---TFRR-----T 214
DB 416 ILIGLVAIIILLILLIIMLM-----WRHWRRLSKARRVLEELTVHLSVPGDTILIN 471
QY 215 PRGEQVPP-----VSPODLL 232
DB 472 NRPGRPEPPYQEPNRPGRTPPHSAPCVNGSALL 506
RESULT 11
CNG4_BOVIN STANDARD; PRT; 1394 AA.
ID AC Q28181; Q28082; Q03861;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 240 kDa protein of rod photoreceptor CNG-channel [Contains: Glutamic
acid-rich protein (GARP); Cyclic-nucleotide-gated cation channel 4
(CNG channel 4) (CNG-4) (Cyclic nucleotide-gated cation channel
modulatory subunit)].
GN CNGB1 OR CNGC4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
ON NCBI_TaxID=9913;
RX MEDLINE=9600859; PubMed=7546742.
RA Goetschen H.G., Illing M., Seifert R., Sesti F., Williams A.,
RA Koerschen S., Colville C., Mueller F., Dose A., Godde M., Molday L.,
RA Kaupp U.B., Molday R.S.;
RT "A 240 kDa protein represents the complete beta subunit of the cyclic
nucleotide-gated channel from rod photoreceptor.";
RL Neuron 15:627-636(1995).
RN
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=9609859; PubMed=8626431.
RA MEDLINE=96198098; PubMed=8626431;
RX Biel M., Zong X., Ludwig A., Sauter A., Hofmann F.;
RT "Molecular cloning and expression of the modulatory subunit of the
cyclic nucleotide-gated cation channel.";
RL J. Biol. Chem. 271:6349-6355(1996).

[3]
 RN SEQUENCE OF 1-590 FROM N.A.
 RC TISSUE-RETINA;
 RA Sugimoto Y., Yatsunami K., Tsujimoto M., Khorana H.G., Ichikawa A.;
 RL Submitted (XXX-1991) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBMITT: FORMS FUNCTIONAL HETEROLOGICOMERIC CHANNELS WITH CNG3.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: CNG4C (SHOWN HERE), CNG4D
 CC AND CNG4E; ARE PRODUCED BY ALTERNATIVE SPLICING. CNG4D IS BY FAR
 CC THE MOST FREQUENT FORM (CNG4D:CNG4C:CNG4E = 20:2:1) IN TESTIS.
 CC -1- TISSUE SPECIFICITY: RETINA, TESTIS, KIDNEY, HEART, AND BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL: X89626; CAA61769.1; -;
 DR EMBL: X94707; CAA64367.1; -;
 DR EMBL: M61185; AAA30536.1; -;
 DR InterPro: IPR000636; M-channel.nlg
 DR InterPro: IPR000595; CNMP_binding.
 DR Pfam: PF00027; CNMP_binding; 1.
 DR Pfam: PF00520; Ion_trans; 1.
 DR SMART: SM00100; CNMP; 1.
 DR PROSITE: PS00888; CNMP_BINDING_1; 1.
 DR PROSITE: PS00889; CNMP_BINDING_2; 1.
 DR PROSITE: PS50042; CNMP_BINDING_3; 1.
 DR PROSITE: PS50042; CNMP_BINDING_3; 1.
 DR Ionic channel; Ion transport; CNMP-binding; Transmembrane;
 KM Multigene family; Alternative splicing.
 FT CHAIN 1 590
 FT DOMAIN 1 767
 FT TRANSMEM 768 786
 FT DOMAIN 787 800
 FT TRANSMEM 801 819
 FT DOMAIN 821 844
 FT TRANSMEM 845 864
 FT TRANSMEM 865 901
 FT TRANSMEM 902 924
 FT TRANSMEM 925 968
 FT TRANSMEM 969 988
 FT DOMAIN 1072 1093
 FT TRANSMEM 1094 1394
 FT DOMAIN 1081 1129
 FT BINDING 1141 1141
 FT BINDING 1141 1153
 FT CARBOHYD 1067 1067
 FT VARSPLIC 515 532
 FT VARSPLIC 522 530
 FT CONFLICT 341 341
 FT CONFLICT 454 465
 FT CONFLICT 482 482
 FT CONFLICT 499 499
 FT CONFLICT 572 590
 FT CONFLICT 1283 1283
 FT CONFLICT 1289 1289
 FT CONFLICT 1336 1336
 FT CONFLICT 1338 1338
 SO SEQUENCE 1394 AA; 155064 MW; EE6DA559BE3744A7 CRC64;
 Query Match 7.0%; Score 86.5; DB 1; Length 1394;
 Best Local Similarity 24.6%; Pred. No. 18;
 Matches 35; Conservative 13; Mismatches 53; Indels 41; Gaps 5;
 QY 115 PPSGLRFVQNTISRL-----QETSDVLAALKWITRONSRCL 154

DB 163 PGFWLLRWEQNLEKMLPPPKISEGWRDEPDALGPEPPGALDKPMLQAQ----- 216
 QY 155 ELQCCPDSSTLPWPSPRPLEATAPAPQPLLLLPVGLLLLAAMCLHMQRTRRT 214
 DB 217 -----ESSSLRPGGPEEPEEP-EPQPTIOASSLPPODSARLMMILH--RLMAL 267
 QY 215 PRP-----GEQVPPVSPDOL 230
 DB 268 PVPVIRKGGEQESDAPVCDV 289
 RESULT 12
 SSGP_VOLCA STANDARD; PRT; 485 AA.
 AC P21997;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Sulfated surface glycoprotein 185 (SSG 185).
 OS Volvox carterl.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Volvocaceae; Volvox.
 OX NCBI_TaxID=3067;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=F. Nagariensis / HK10;
 RA MEDLINE=90094551; Pubmed=2689458;
 RX Ertl H., Menzies R., Wenzl S., Engel J., Sumner M.;
 RT "The extracellular matrix of Volvox carterl: molecular structure of
 RT the cellular compartment";
 RL J. Cell Biol. 109:3493-3501(1989).
 CC -1- FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS
 CC INSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A
 CC DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS THE
 CC MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C32 STRUCTURE). THE
 CC COVALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS
 CC RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.
 CC -1- PTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF
 CC HYDROXYPROLINE RESIDUES.
 CC -----
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 CC -----
 DR EMBL: X51616; CAA35953.1; -;
 DR PIR: A33647; A33647.
 KM Glycoprotein; Sulfation; Hydroxylation.
 FT DOMAIN 228 340
 FT DOMAIN 260 295
 FT POLY-PRO.
 SO SEQUENCE 485 AA; 50436 MW; A52216400A031421 CRC64;
 Query Match 6.9%; Score 86; DB 1; Length 485;
 Best Local Similarity 29.2%; Pred. No. 5.9;
 Matches 21; Conservative 3; Mismatches 22; Indels 26; Gaps 1;
 QY 160 PDSSTLPWPSPRPLEATAPAPQPLLLLPVGLLLLAAMCLHMQRTRRRPGE 219
 DB 275 PPSPPPPPPPPPPPPPPPPPPSP-----RKPPSPSP 308
 QY 220 QVPPVSPDOLL 231
 DB 309 PVPVIRKGGEQESDAPVCDV 320
 RESULT 13
 ATFS_HUMAN STANDARD; PRT; 282 AA.
 AC Q9Y2D1; Q9UN03;

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 27, 2003, 18:25:46 ; Search time 19 Seconds
(Without alignments)
1189.031 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242
Sequence: 1 MVLAPAWSPPTVLLLLLL.....RPEQVPPVPSDOLLVER 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 1242 | 100.0 | 235 | 2 I38440 | flt3 ligand - huma |
| 2 | 864.5 | 69.6 | 245 | 2 S43293 | FLT3/FLK2 ligand (|
| 3 | 834 | 67.1 | 178 | 2 I39076 | flt3 ligand altern |
| 4 | 768.5 | 61.9 | 231 | 2 A49265 | flt3/Flk2 ligand |
| 5 | 606.5 | 48.8 | 220 | 2 S43291 | FLT3/FLK2 ligand (|
| 6 | 606.5 | 48.8 | 220 | 2 I58343 | flt3 ligand isofor |
| 7 | 93 | 7.5 | 1217 | 2 T22672 | hypothetical prote |
| 8 | 92 | 7.4 | 661 | 1 TNBE12 | 74k alpha trans-in |
| 9 | 89.5 | 7.2 | 474 | 1 T19543 | hypothetical prote |
| 10 | 89 | 7.2 | 387 | 1 I48201 | adhalin - golden h |
| 11 | 89 | 7.2 | 793 | 1 S60735 | splicing factor SF |
| 12 | 88.5 | 7.1 | 238 | 2 AB1990 | hypothetical prote |
| 13 | 88.5 | 7.1 | 1386 | 2 T00257 | hypothetical prote |
| 14 | 88 | 7.1 | 753 | 2 J00532 | OP protein - Kenne |
| 15 | 87.5 | 7.0 | 479 | 1 A33290 | protein-tyrosine-p |
| 16 | 87 | 7.0 | 910 | 2 A53337 | tyrosine kinase re |
| 17 | 86.5 | 7.0 | 590 | 2 A40437 | glutamic acid-rich |
| 18 | 86 | 6.9 | 299 | 2 T17832 | hypothetical prote |
| 19 | 86 | 6.9 | 485 | 2 A33647 | sulfated surface g |
| 20 | 86 | 6.9 | 746 | 2 T28004 | hypothetical prote |
| 21 | 85 | 6.8 | 289 | 2 A87646 | hypothetical prote |
| 22 | 85 | 6.8 | 366 | 2 A37374 | FC gamma (Igg) rec |
| 23 | 84 | 6.8 | 263 | 2 T03162 | gamma-globulin 6 |
| 24 | 84 | 6.8 | 757 | 2 A39283 | legumain protein 6 |
| 25 | 83.5 | 6.7 | 199 | 2 E75630 | hypothetical prote |
| 26 | 83.5 | 6.7 | 530 | 2 A45690 | transactivator EBN |
| 27 | 83 | 6.7 | 1509 | 2 T19486 | hypothetical prote |
| 28 | 82.5 | 6.6 | 418 | 2 T19800 | hypothetical prote |
| 29 | 82.5 | 6.6 | 426 | 2 I36948 | Ig epsilon-chain - |

| | | | | | |
|----|------|-----|------|----------|--------------------|
| 30 | 82.5 | 6.6 | 512 | 2 D40829 | activin receptor 1 |
| 31 | 82.5 | 6.6 | 513 | 2 J01484 | activin receptor p |
| 32 | 82 | 6.6 | 106 | 2 T06479 | proline/leucine-ri |
| 33 | 82 | 6.6 | 854 | 2 T23837 | hypothetical prote |
| 34 | 81.5 | 6.6 | 485 | 2 C75460 | hypothetical prote |
| 35 | 81.5 | 6.6 | 488 | 2 S13423 | stromelysin 3 (EC |
| 36 | 81.5 | 6.6 | 958 | 2 T13593 | hypothetical prote |
| 37 | 81.5 | 6.6 | 1119 | 2 T50995 | related to cytoske |
| 38 | 81 | 6.5 | 196 | 2 B48232 | cysteine-rich exte |
| 39 | 81 | 6.5 | 209 | 2 A48232 | cysteine-rich exte |
| 40 | 81 | 6.5 | 294 | 2 A12016 | hypothetical prote |
| 41 | 81 | 6.5 | 388 | 2 S15591 | probable transpos |
| 42 | 81 | 6.5 | 428 | 1 EHHU | Ig epsilon chain C |
| 43 | 80.5 | 6.5 | 636 | 2 JW0047 | class I cytochrome |
| 44 | 80.5 | 6.5 | 1176 | 2 T49482 | hypothetical prote |
| 45 | 80.5 | 6.5 | 1306 | 2 T13592 | hypothetical prote |

ALIGNMENTS

RESULT 1
I38440
flt3 ligand - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence-revision 29-May-1998 #text-change 01-Dec-2000
C:Accession: I38440; I39075; S43292
R:Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe
Blood 83, 2795-2801, 1994
A:Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor fo
A:Reference number: I38440; MUID:94235842; PMID:8180375
A:Accession: I38440
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-235 <RES>
A:Cross-references: EMBL:U03856; NID:9494978; PIDN:AA19825.1; PID:9494979
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581; PMID:7566977
A:Accession: I39075
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-235 <RES>
A:Cross-references: EMBL:U29874; NID:91072036; PIDN:AA90949.1; PID:91072037
R:Hannun, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.;
felt, A.; Muench, M.; Kellner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik
Nature 368, 643-648, 1994
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopo
A:Reference number: S43290; MUID:94195428; PMID:8145851
A:Accession: S43292
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-71, 'A', 73-235 <HAN>
A:Cross-references: GB:U04806; NID:9483844; PIDN:AA1999.1; PID:9483845
A:Note: the authors translated the codon AGT for residue 25 as Met
C:Genetics:
A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3
Query Match 100.0%; Score 1242; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 5, 4e-99;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MVLAPAWSPPTVLLLLSSGSGTQDCSFQHSPISSDFAVKRLRELDVLLDYPYTV 60
Db 1 MVLAPAWSPPTVLLLLSSGSGTQDCSFQHSPISSDFAVKRLRELDVLLDYPYTV 60
OY 61 ASNLDEELCGGLMRLVLAORMERLKTIVAGSKMGLERVNTLHFVTKCAFOPPSCL 120
Db 61 ASNLDEELCGGLMRLVLAORMERLKTIVAGSKMGLERVNTLHFVTKCAFOPPSCL 120
OY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLLELQCPDPSSTLPWMSRPRLPATPT 180
Db 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLLELQCPDPSSTLPWMSRPRLPATPT 180

Db 121 RYVQNTSIRLLQESSEQLVAKPMTITQNFSCLELQCPQSSSLPPMPSRPLLEATAPT 180

Qy 181 APQPPULLLLLLPYGULLLAAMKCLHMQRTRRTPRPGEGVPPVPSPQDILLVNH 235

Db 181 APQPPULLLLLLPYGULLLAAMKCLHMQRTRRTPRPGEGVPPVPSPQDILLVNH 235

RESULT 2

FLT3/FLT2 ligand (clone S109) - human
 C:Species: Homo sapiens (man)
 C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
 C:Accession: S43293
 R:Hannum, C.; Cuipepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Felt, A.; Muench, M.; Kelnier, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A.
 A:Title: Ligand for FLT3/FLT2 receptor tyrosine kinase regulates growth of haematopoietic
 A:Reference number: S43290; MUID:94195428; PMID:8145851
 A:Accession: S43293
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1245 <HAN>
 A:Note: The authors translated the codon AGT for residue 25 as Met

RESULT 3

Flt3 ligand alternatively spliced isoform - human
 C.Species: Homo sapiens (man)
 C.Date: 29-May-1998 #sequence-revision 29-May-1998 #text-change 21-Jul-2000
 C.Accession: I39076
 R.Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
 Oncogene 11, 1165-1172, 1995
 A.Title: Structural analysis of human and murine flt3 ligand genomic loci.
 A.Reference number: I39075; MIMD:56032581; PMID:7566977
 A.Accession: I39076
 A.Status: preliminary; translated from GR/EMBL/DBJ
 A.Molecule type: DNA
 A.Residues: 1-178 <RES>
 A.Cross-references: EMBL:U029874; NID:g1072036; PIDN:AAA90950.1; PID:g1072038
 C.Genetics:
 A.Introns: 11/3; 48/3; 66/3; 114/3; 161/1

| Db | 1 | MTVLAPASPTTYLLLLLLLLSSGSGTQDCFSQHSPISSDEAVYIRELSYLLLDYDPVAV | 60 |
|----|-----|---|-----|
| Qy | 61 | ASNLODELTGGWRIYLAQWMERIKTVAGSKMOGLLERPNEIHHVTCAQRPSPCL | 120 |
| Db | 61 | ASNLODELTGGWRIYLAQWMERIKTVAGSKMOGLLERPNEIHHVTCAQRPSPCL | 120 |
| Qy | 121 | RFVQVTSIRLLQETSQGLVALKPMVITQNSRSCLELQCP | 160 |
| Db | 121 | RFVQVTSIRLLQETSQGLVALKPMVITQNSRSCLELQCP | 160 |

RESULT 4

flt3/fk-2 ligand precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence.revision 13-Jan-1995 #text_change 08-Oct-1999
C:Accession: A49265; I49347, I49346; S43290
R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Holl
Cell 75, 1157-1167, 1993
A:Title: Molecular cloning of a ligand for the flt3/fk-2 tyrosine kinase receptor: a
A:Reference number: A49265; MUID:94084791; PMID:7505204
A:Accession: A49265
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-231 <LR>
A:Cross-references: GB:I23636; NID:g439441; PIDN:AAA39436.1; PID:g439442
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581; PMID:7566977
A:Accession: I49347
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-163, 'G', 165, 'HYAG' <RES>
A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041
A:Accession: I49346
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-197, 'L', 198-231 <RE2>
A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040
R:Hannun, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.;
Felt, A.; Muench, M.P.; Kelnier, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik
Nature 368, 643-648, 1994
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic
A:Reference number: S43290; MUID:94195428; PMID:8145851
A:Accession: S43290
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-197, 'L', 198-231 <HAN>
A:Experimental source: clone T110
A:Note: the sequence from Fig. 2c is inconsistent with that from Fig. 2a in having 4-
C:Genetics:
A:Introns: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3
C:Keywords: transmembrane protein

| | Query Match | Similarity | 61.9% ; Score 768. -5; DB 2; Length 231; |
|----|-------------|---|--|
| | Best Local | Similarity | 70.3% ; Pred. No. 1,8e-58; |
| | Matches | 163; Conservative | 17; Mismatches 43; Indels 9; Gaps 4; |
| QY | 1 | MTVLAPAWSP--TYYLLLLLLLSSGSGTGDGCSFQHSPISSDPAVKIRELDYLDQDPVT | 59 |
| | | : : : : : : : : : : : : : : : | |
| DB | 1 | MTVLAPAWSPNSSLLLLLLLLLLSPCLRGTPDCCYFHSHPSSNFVKFRELDHLLKDYPT | 60 |
| QY | 60 | VASNIQDEBELCGGLRLVLAQRMMERLKTAVGSKMOGLELVNNEIHFPVTKCAQPPESC | 119 |
| | | : : : : : : : : : : : : : : : : : : : : : : : : : | |
| DB | 61 | VAVNIQDEKHCKALMSLFLAQRMIEQLKTAVGSKMQLLELVNNEIHFPVTSCTQPLEC | 120 |
| QY | 120 | LRFVQTNISRLQESQGLAPMIFR--QNFSRCLTEQCPQSSSTLRPPWSPRLPEAT | 177 |
| | | : : : : : : : : : : : : : : : : : : : : : : : : : | |
| DB | 121 | LRFVQTNISHLKDTQYLLALAKPCIGACQNFPSRCLELVQCPQSSSTLRLPPRSIALEAT | 180 |
| QY | 178 | APVAPQPE--LLLLLLLVGLLLLLAAMWCLQMQRTRRRTPRGEQVPPVSP | 227 |

OY 124 QTNISRLQETSEQLVAKPMITRONFSRCLELOCOPDSSLTPEPPMSP-RPLEATAPAP 182
 Db 198 NSRYRGICQELRLALGAVQYKYM--YFMR-----PDDETPNSPDTRIRVQEIATAT 247
 OY 183 QPPLLILLLLPVGLLLLAAMCLHWQTRRRTPRGQVPPVPSPODL 231
 Db 248 GYGMWMLFELVD-----ARVCRHLKLOFRIRKGRASV----IPDDL 287

RESULT 9

T19543

hypothetical protein C28D4.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T19543

R:McMurray, A.

Submitted to the EMBL Data Library, November 1996

A:Reference number: Z19139

A:Accession: T19543

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-474 <MIL>

A:Cross-references: EMBL:Z82259; PDB:CA05129.1; GSPDB:GN00022; CESP:C28D4.2

A:Experimental source: clone C28D4

C:Genetics:

A:Gene: CESP:C28D4.2

A:Map position: 4

A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Query Match

Best local similarity 7.2%; Score 89.5; DB 2; Length 474;

Matches 59; Conservative 29; Mismatches 82; Indels 75; Gaps 15;

OY 27 TDQC-----SFQHS-PISSDFAVKIREL-SDYLQDYPVTVASNLQDELGGIMRL 76
 Db 65 TDCVDLKVFSKFSKSSAPISGELFPAFLCAKYL-----GCAMRK 106
 OY 77 VLAQRMERKITYAGSMQGLLERNTEHFVVKCAQPPSCIR-FVQTNISRLQET- 134
 Db 107 VKLEEF-RIRATIGG-MSNLLFLVELPAH-LPPIQMEPKALLRVQSDIDLLSESV 162
 OY 135 -----SEDLVAKPMITRONFSRCLELOC-----OPDSSLTPEPPMSP-RPLEATA 178
 Db 163 VFTLLSRNLGPKMLGVPGRGREFQIFPSRALQCLEISKGLSLPIYARVHTLDAPI 222
 OY 179 PTAPQPLLILLLLPVGLLLLAAMCLHWQTRRRTP--RPGE-----QVPPVPSPOD 229
 Db 223 PKBPQ-----TLQTAQWLRRF---KKPAGERPIEMVLTQAKVPSDYEST 266
 OY 230 LLVE 234
 Db 267 ITVAQ 271

RESULT 10

I48201

adhalin - golden hamster

C:Species: Mesocricetus auratus (golden hamster)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Jun-2000

C:Accession: I48201

R:Roberts, S.L.; Campbell, K.P.

FEBS Lett. 364, 245-249, 1995

A:Title: Adhalin mRNA and cDNA sequence are normal in the cardiomyopathic hamster.

A:Reference number: I48201; MID:95278335; PMID:7758576

A:Accession: I48201

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-387 <RES>

A:Cross-references: EMBL:U21677; MID:9726481; PDB:AAA81645.1; PID:9726482

C:Superfamily: mouse adhalin

Query Match 7.2%; Score 89; DB 2; Length 387;
 Best local similarity 23.4%; Pred. No. 4.8;

Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps 14;

OY 11 TTVLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDYLQDYPVTVASNLQDELGC 70
 Db 115 TTRQRLILLI-----EDEGRPLPYQAEFLVRSHVEVL-----PSTANFL--TAL 161
 OY 71 GGLMRL-----VLAQRMERKITYAGSMQGLLERNTEHFVVKCAQPPSCIR-FVQTNISRLQETSEQLVAKPMITRONFSRCLELOCOPD 110
 Db 162 GGLMELGELQLNLTMSALDRGVRPLPIEGRKEGVYIKVGSATPFSGCLMKVASPPSYAR 221
 OY 111 CAFQPP--SC-----LRFVQTNISRLQETSEQLVAKPMITRONFSRCLELOCOPD 161
 Db 222 CAQGQPPLLSCYSLAPHFVRWDMCNVSLVDKSVPEPLD-----EVPFPGD 266
 OY 162 SSTLPPEMSPRPLEAT-----APTAPQPLLILLLLPVGLLLLAAMC----- 204
 Db 267 GILEHDPFCPPPEATGRDLALVTLVPLVALL--TLLVALIMCRRREGQLKR 323
 OY 205 -----LHMQTRRRTPRP-----GECVPP-VSPQ-DLL 231
 Db 324 MATSDIQMVHCHTGHNTTEELROMAARREVPRPLSTLPMENVRGRLPERVDSAGVPLI 383
 OY 232 LVEH 235
 Db 384 LDQH 387

RESULT 11

S60735

splicing factor SF3a 120K chain - human

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C:Accession: S60735; S60733

R:Kraemer, A.; Mulhauser, F.; Wersig, C.; Groening, K.; Bilbe, G.

RNA 1, 260-272, 1995

A:Title: Mammalian splicing factor SF3a120 represents a new member of the SUPR family

A:Reference number: S60733; MID:96079958; PMID:7489498

A:Accession: S60735

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-793 <KRA>

A:Cross-references: EMBL:X85237; MID:9899297; PDB:CAA59494.1; PID:9899298

A:Accession: S60733

A:Molecule type: protein

A:Residues: 51-62; 82-94; 270-275; 397-414; 448-463 <KRA>

A:Gene: GDB:SF3A120; PRP21; SAP114

A:Cross-references: GDB:9955873

A:Map position: 22q12.1-22qter

C:Superfamily: human splicing factor SF3a 120K chain; ubiquitin homology

C:Keywords: pre-mRNA splicing

E:714-790/Domain: ubiquitin homology <DBH>

Query Match 7.2%; Score 89; DB 1; Length 793;

Best local similarity 22.3%; Pred. No. 11; Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

OY 4 LAPAMSPYTVLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDYLQDYPVTVASN 63
 Db 401 LPPAPAPDEYLV-----SPITGE--KI-----PASK 424
 OY 64 LQDELQGGIMRLVLAQRME-RLKTV-----AGSMQGLLERNTEHFVVKCAQPPSCIR-FVQTNISRLQETSEQLVAKPMITRONFSRCLELOCOPD 107
 Db 425 MQEHRIG-----LIDPRWLEQDRSTIREKQSDDEVYAPGLDISSLSKOLAER-RDIFG 478
 OY 108 VTRCA-----FQPPSCIRF-----VQTNISRLQETSEQLVAKPMITRONFSRCLELOCOPD 145
 Db 479 VETALGKKTGEEBQIKPEKAVWMDGSSMARTQAQANIT--LQFQELAHKKKGLV 536
 OY 146 ----TRQNF--SRCLELOC-----DSSTLP-----PPMSPRPLEAT--APT 180
 Db 537 PEDDTKEIKIPSKPNEIQQPPPPSSATNIPSSAPITSVPRPTMPVPVKTIVSAAVAV 596

OY 181 APOPELLELLLPVGLLLAAWCLHMQR-----RRTPREGQVPP---VSP 227
 Db 597 MPRPMASVYRLPPGVIAVMPRIIAVRINVMPSAPPIAARPPPIVPAFVAP 656

RESULT 12

AB1990
 hypothetical protein all1471 [Imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C:Accession: AB1990
 R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, S.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AB1990

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-238 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA077837.1; PID:g17135292; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all1471

Query Match 7.1%; Score 88.5; DB 2; Length 238;
 Best Local Similarity 20.8%; Pred. No. 3;
 Matches 44; Conservative 32; Mismatches 59; Indels 77; Gaps 9;

OY 34 HSPISDFAVKIRELSDYLQDY--PVTVASNLQDELQGLMRLVLAQRMERLTV 90
 Db 84 HSKRTTYESINEVCNOYLKSEKPLVLI-----QILG-W---SGLMKYKTV 131

OY 91 GSKMGLLEVNTEHIVTKCAQPPSCIRFYQFNISRLQ-----EISEQ 137
 Db 132 DDDDTDISPISSTEV-----VVRKIPKVIETPKIVKPKQTEKIDLES 174

OY 138 LVALKPWITRQNSRCLQCOPODSTLPPPM---SPRPLEATAPAPOPPLLLLPV 194
 Db 175 PGLKRP--TKPIPKLIEPKSSESKMLQRPIDSPKPIKNSQPEAKRYV----- 223

OY 195 GLLLLAAWCLHMQRTRRTPRREGQVPPVPS 226
 Db 224 -----EPPKPMERVPKPPS 237

RESULT 13
 T00257
 hypothetical protein KIAA0476 - human
 C:Species: Homo sapiens (man)
 C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000

C:Accession: T00257

R:Seiki, N.; Ohita, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.

DNA Res. 4, 345-349, 1997

A:Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human

A:Reference number: 214085; MUID:98116662; PMID:9455484

A:Accession: T00257

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1386 <SEK>

A:Cross-references: EMBL:AB007945; NID:g3413913; PIDN:BA32321.1; PID:g3413914

A:Experimental source: brain

C:Genetics:

A:Note: KIAA0476

Query Match 7.1%; Score 88.5; DB 2; Length 1386;
 Best Local Similarity 23.1%; Pred. No. 23;
 Matches 53; Conservative 28; Mismatches 85; Indels 63; Gaps 12;

OY 21 SSGLSGQDPSFOHSPISDFAVKIRELSDYLQDYVTVASNLQDELQ-----GGLMRL 76
 Db 1104 SAGASGSKADVPVPGP-----GPVLSDRRLCLA--LDEPOLCNGHMGASRR 1148

OY 77 VLAQRMERLKTAVGSKMGLLEVNTEHIVTKCAQPPSCIRFYQFNISRLQENSE 136
 Db 1149 VESGAMAYLSPLVLRKELSEVENEGSEV-----LALPELSAPPIIWMILMTFQRL-- 1201

OY 137 QLVALKPWITRQNSRCLQCO--PDSTLPPPM--SPRPLEA-----TAPAPOP 185
 Db 1202 RLPSILPGLVLAS-----CDGPPSHSQAPSPMLTPDPASVQVRLMDVLTTPPNNSCPP 1253

OY 186 LLLLLLPVGLLLAAWCLHMQRTRRTPRREGQVPPVPSQDLLVE 234
 Db 1254 LVYL-----WRVHSQ--IPQRVWVG---PVPAISLVLALLE 1284

RESULT 14

J00532
 OP protein - Kennedy yellow mosaic virus
 C:Species: Kennedy yellow mosaic virus
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999

C:Accession: J00532

R:Ding, S.; Keese, P.; Gibbs, A.

J. Gen. Virol. 71, 925-931, 1990

A:Title: The nucleotide sequence of the genomic RNA of Kennedy yellow mosaic tymovir

A:Reference number: J00532; MUID:90218040; PMID:2324710

A:Accession: J00532

A:Molecule type: mRNA

A:Residues: 1-753 <DIN>

A:Cross-references: GB:000637; NID:g221969; PIDN:BA00531.1; PID:d100986; PID:g22197

A:Experimental source: strain Jervais Bay isolate

Query Match 7.1%; Score 88; DB 2; Length 753;
 Best Local Similarity 22.3%; Pred. No. 12;
 Matches 41; Conservative 19; Mismatches 58; Indels 66; Gaps 7;

OY 100 RVNTEHIVTKCAQPPSCIRF-----VQTNIS-----RLQENSEQVLAKPWTR 147
 Db 420 RLSTQPPSSPQSTSSPPSPPTDASGIQPLASPPSKRKSLEPHSHQ---PPSHK 475

OY 148 QNFSR-----CLELCOPODSTLPPPMSPRPLEATAPAPOPPLLLLPV----- 193
 Db 476 RNLRRHSLPLLLPIHPIKTTQPPHNPVQP--TAGPTPHPPPTKPIPLHPKSOERHNSP 533

OY 194 -----VGLLLAAWCLHMQRTRRTPRREGQVPPVPS 226
 Db 534 PPVDFHDCQPSPTSHVGVYRRLGSGISLPFKLAFW-----RRSPNPARHLPPPPP 586

OY 227 PQDL 230
 Db 587 PRKL 590

RESULT 15
 A32290
 protein-tyrosine-phosphatase (EC 3.1.3.48) cdcs2 homolog string - fruit fly (Drosophila)

C:Species: Drosophila melanogaster

C:Date: 05-Oct-1989 #sequence_revision 25-Apr-1997 #text_change 11-Jun-1999

C:Accession: A32290

R:Edgar, B.A.; Farrell, P.H.

Cell 57, 177-187, 1989

A:Title: Genetic control of cell division patterns in the Drosophila embryo.

A:Reference number: A32290; MUID:89195217; PMID:2702688

A:Accession: A32290

A:Molecule type: mRNA

A:Residues: 1-479 <EDG>

A:Cross-references: GB:M24909; NID:g158507; PIDN:AAA28916.1; PID:g158508

R:Jimenez, J.; Alphey, L.; Nurse, P.; Glover, D.M.

EMBO J. 9, 3565-3571, 1990

A:Title: Complementation of fission yeast cdc2(1s) and cdc25(1s) mutants identifies t

A:Reference number: S12008; MUID:91006056; PMID:2120044

A:Accession: S12008

A:Molecule type: mRNA

A:Residues: 1-227, 'A', 229-479 <JIM>

A:Cross-references: EMBL:X57495; NID:g7706; PIDN:CAA40732.1; PID:g7707

